

This Page Is Inserted by IFW Operations
and is not a part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

**As rescanning documents *will not* correct images,
please do not report the images to the
Image Problems Mailbox.**

(19)



Europäisches Patentamt
European Patent Office
Office européen des brevets



(11)

EP 0 791 655 A2

(12)

EUROPEAN PATENT APPLICATION

(43) Date of publication:
27.08.1997 Bulletin 1997/35

(51) Int Cl.⁶: **C12N 15/52, C12N 9/00,
C12N 15/63, C12P 17/08,
C12P 19/62**

(21) Application number: **97301056.4**

(22) Date of filing: **19.02.1997**

(84) Designated Contracting States:
**AT BE CH DE DK ES FI FR GB GR IE IT LI LU NL
PT SE**

(30) Priority: **22.02.1996 US 12078**

(71) Applicant: **ELI LILLY AND COMPANY**
Indianapolis, Indiana 46285 (US)

(72) Inventors:
• **Dehoff, Bradley Stuart**
Indianapolis, Indiana 46214 (US)

• **Kuhstoss, Stuart Allen**
Indianapolis, Indiana 46256 (US)
• **Rosteck, Paul Robert, Jr.**
Indianapolis, Indiana 46237 (US)
• **Sutton, Kimberly Lynn**
New Palesatine, Indiana 46163 (US)

(74) Representative: **Tapping, Kenneth George**
Lilly Industries Limited
European Patent Operations
Erl Wood Manor
Windlesham Surrey GU20 6PH (GB)

(54) **Polyketide synthase genes**

(57) A DNA molecule isolated from *Streptomyces*

fradiae encodes the multi-functional proteins which direct the synthesis of the polyketide tylactone.

EP 0 791 655 A2

Description

The present invention relates to DNA molecules responsible for encoding the multi-functional proteins that direct the biosynthesis of polyketide compounds, the products encoded by said DNA molecules, recombinant DNA expression vectors, and transformed microbial host cells.

Polyketides are a family of compounds that include a large number of structurally and functionally diverse natural products. For example, the polyketides provide the structural backbone for compounds that exhibit a variety of biological activities, such as, antibiotic, antitumor, and immunosuppressive agents.

Although the polyketides are quite diverse as indicated, they share a common mechanistic scheme of biosynthesis.

The polyketides are synthesized by the successive condensation of small carboxylic acid residues followed by variable reduction steps at the resulting β -keto carbon (i.e., β -carbonyl) moiety in a process that is similar to the synthesis of fatty acids. The iterative synthetic process for many of these polyketides is controlled by a complex of large, multi-functional polypeptides that have distinct sites for the variety of activities that are required.

The general scheme for polyketide biosynthesis has been reviewed, for example, in Hopwood and Sherman, *Annu. Rev. Genet.*, 1990, 24:37 and Katz and Donadio, *Annu. Rev. Microbiol.*, 1993, 47:875.

Naturally-occurring DNA sequences that encode the polyketide synthase enzymes have generally been found to be organized into repeated subunits, or modules, each of which encodes all the activities required in a single round of synthesis, which includes the condensation step itself and the post-condensation processing steps. Each activity is associated with a distinct site, which contributes to the specificity for the particular carboxylic acid building block that is incorporated at each condensation step, or which dictates the particular post-condensation processing functions that will be executed.

For example, PCT publication WO 93/13663 describes the organization of the gene encoding the polyketide synthase of *Saccharopolyspora erythraea*. The gene is organized in modules, with each module effecting one condensation step. The precise sequence of chain growth and the processing of the growing chain is determined by the genetic information in each module. This PCT application describes an approach for synthesizing novel polyketide structures by manipulating in several ways the DNA governing the biosynthesis of the cyclic lactone framework. In order to adapt this methodology to other polyketides, however, the DNA molecules directing the biosynthetic processing must first be isolated.

The present invention is directed to the DNA sequence for the gene cluster responsible for encoding tylactone synthase, the building machinery of tylactone, which is the basic building block of tylosin. As a result, the present invention enables modification of the DNA sequence so as to alter the type of carboxylic acids incorporated, the number of carboxylic acids incorporated, the post-condensation reactions performed, or any combination thereof, thereby resulting in novel tylosin-related polyketides.

The present invention provides a DNA molecule comprising an isolated DNA sequence that encodes a tylactone synthase domain. Thus, the present invention provides the DNA molecule of SEQ ID NO:1 and DNA molecules that contain submodules thereof. The present invention also provides the products encoded by said DNA molecules, recombinant DNA expression vectors, and transformed microbial host cells.

Figure 1 is a map of the tylactone polyketide synthase region (*tylG*) of the *Streptomyces fradiae* DNA (~45 kb). Distances in kb are relative to the beginning of *tylG*. Open reading frames (ORFs) are indicated by arrows. Restriction sites are denoted as follows:

E - *EcoRI*
B - *BamHI*

Predicted functional domains are labeled as follows:

ACP - acyl carrier protein
AT - acyltransferase
DH - dehydratase
ER - enoylreductase
KR - ketoreductase
KR' - ketoreductase-like domain predicted to be inactive
KS - ketosynthase
KS' - ketosynthase-like domain in which a glutamine residue is present in the position occupied by an active site cysteine in a normal ketosynthase
TE - thioesterase.

Figure 2 depicts the biosynthetic pathway for tylactone synthesis.

Figure 3 is a map of the two clones that span the whole region of the *tylG* DNA.

Figure 4 is a map of the *srnG* region of the *Streptomyces ambofaciens* DNA. Distances in kb are relative to the beginning of *srnG*. Open reading frames are indicated by arrows. The *srnG* DNA (0-42 kb) is the platenolide polyketide synthase region. Restriction sites are denoted as above with additions as follows:

AP - *Apal*
G - *BglII*
K - *KpnI*
P - *PstI*
X - *XhoI*

Predicted functional domains are labeled as above.

Figure 5 demonstrates the biosynthetic pathway for platenolide synthesis.

Figure 6 is a map of the two clones that span the whole region of the *srnG* DNA.

Polyketides are a large class of structurally and functionally diverse natural products. A common feature of compounds in this class is that their synthesis is accomplished under the direction of a complex of multi-functional peptides, termed a "polyketide synthase." Molecular genetic analysis of polyketide synthase genes has revealed two distinct classes of enzymes operating for different polyketides: 1) the aromatics, which are made through an essentially iterative process, and 2) the complex polyketides, which comprise several repeats of the same activities arranged in few very large polypeptides.

Among the complex polyketide synthase genes, a polyketide synthase includes enzymatic and regulatory activities responsible for exercising substrate specificity, catalyzing the condensation of small carboxylic acid building blocks (in the form of coenzyme A thioesters) to a growing polyketide carbon chain, and catalyzing the post-condensation processing reactions at the β -carbonyl functional group that results from the condensation reaction.

The condensation reaction requires several activities including acyl carrier protein (ACP), β -ketosynthase (KS), and acyltransferase (AT). Once a condensation has occurred, the resulting β -carbonyl functional group may be modified. Post-condensation activities that may be involved include β -ketoreductase (KR), dehydratase (DH), and enoylreductase (ER). Polyketide biosynthesis is terminated by a thioesterase (TE) activity. Whether all, some, or none of these activities act after a particular condensation step determines the structure of the final product.

The present invention provides, in particular, the DNA sequence encoding the polyketide synthase responsible for biosynthesis of tylactone, i.e., tylactone synthase. Tylactone itself is the polyketide backbone of the commercially significant antibiotic tylosin. The tylactone synthase DNA sequence, which defines the tylactone synthase gene cluster, directs biosynthesis of the tylactone polyketide by encoding the various distinct activities of tylactone synthase.

The gene cluster for tylactone synthase, like other complex polyketide biosynthetic genes whose organization has been elucidated, is characterized by the presence of several open reading frames (ORFs), each of which contains one or more repeated units termed "modules." A module is defined as the genetic element encoding all of the distinct activities required in a single round of synthesis, i.e., one condensation step and all the β -carbonyl processing steps associated therewith. Each module encodes an ACP, a KS, and an AT activity to accomplish the condensation portion of the synthesis, and selected post-condensation activities to effect β -carbonyl processing. The polypeptides encoded by such modules are termed "synthase units" (SUs).

Each module is further characterized by the inclusion of submodules that are responsible for encoding the distinct activities of tylactone synthase. For purposes of the present invention, the term "submodule" is defined as the portion of the polyketide synthase DNA sequence that encodes a distinct activity, or "domain". Thus, a domain is taken as commonly understood to mean that part of the polyketide synthase polypeptide necessary for a given distinct activity.

Organization of the tylactone synthase gene cluster derived from *Streptomyces fradiae*, is shown in Figure 1. The tylactone synthetic pathway, with indications of the specific carboxylic acid substrates used for each condensation reaction and the various post-condensation activities, is shown in Figure 2.

A preferred DNA molecule comprising the tylactone synthase gene cluster isolated from *Streptomyces fradiae* is represented by SEQ ID NO:1. Other preferred DNA molecules of the present invention include the various open reading frames of SEQ ID NO:1 that encode individual multi-functional polypeptides. These are represented by the following nucleotide residues of SEQ ID NO:1: ORF1 816 to 14234, ORF2 14351 to 19945, ORF3 20010 to 31199, ORF4 31232 to 36067, and ORF5 36249 to 41774. The predicted amino acid sequences of the various peptides encoded by these sequences are shown in SEQ ID NO:2, 3, 4, 5, and 6, respectively.

Yet other preferred DNA molecules of the present invention include the modules that encode the synthase units, which include all the activities necessary for a single round of synthesis. These are represented by the following nucleotide residues of SEQ ID NO:1: Starter Module 942 to 3929, Module 1 3993 to 8471, Module 2 8541 to 13970, Module 3 14411 to 19666, Module 4 20136 to 24611, Module 5 24675 to 30902, Module 6 31337 to 35743, and Module 7 36360 to 40826. The predicted amino acid sequences of the various synthase units encoded by these modules are

represented, respectively, by the following amino acid residues: Starter SU 43 to 1038, SU1 1060 to 2552 and SU2 2576 to 4385 in SEQ ID NO:2; SU3 21 to 1772 in SEQ ID NO:3; SU4 43 to 1534 and SU5 1556 to 3631 in SEQ ID NO:4; SU6 36 to 1504 in SEQ ID NO:5; and SU7 38 to 1526 in SEQ ID NO:6.

Still other preferred DNA molecules include the various submodules that encode the various domains of ty lactone synthase. These submodules are represented by the following nucleotide residues: KS^Q(s) 942 to 2156, AT(s) 2571 to 3557, ACP(s) 3675 to 3929, KS1 3993 to 5264, AT1 5631 to 6617, KR1 7410 to 7949, and ACP1 8220 to 8471 of Module 1 in SEQ ID NO:1; KS2 8541 to 9812, AT2 10260 to 11246, DH2 11319 to 11876, KR2 12861 to 13415, and ACP2 13719 to 13970 of Module 2 in SEQ ID NO:1; KS3 14411 to 15697, AT3 16055 to 17122, DH3 17198 to 17794, KR3 18584 to 19138, and ACP3 19415 to 19666 of Module 3 in SEQ ID NO:1; KS4 20136 to 21404, AT4 21771 to 22757, KR4 23541 to 24077, and ACP4 24360 to 24611 of Module 4 in SEQ ID NO:1; KS5 24675 to 25949, AT5 26292 to 27284, DH5 27360 to 27917, ER5 28767 to 29813, KR5 29829 to 30368, and ACP5 30651 to 30902 of Module 5 in SEQ ID NO:1; KS6 31337 to 32608, AT6 32975 to 33961, KR6 34694 to 35236, and ACP6 35492 to 35743 of Module 6 in SEQ ID NO:1; KS7 36360 to 37631, AT7 37989 to 38987, KR7 39759 to 40313, ACP7 40575 to 40826, and TE7 41235 to 41333 of Module 7 in SEQ ID NO:1.

The predicted amino acid sequences of the various domains encoded by these submodules are represented, respectively, by KS^Q(s) 43 to 447, AT(s) 586 to 914, ACP(s) 954 to 1038, KS1 1060 to 1483, AT1 1606 to 1934, KR1 2199 to 2378, and ACP1 2469 to 2552 in SEQ ID NO:2; KS2 2576 to 2999, AT2 3149 to 3477, DH2 3502 to 3687, KR2 4016 to 4200, and ACP2 4302 to 4385 in SEQ ID NO:2; KS3 21 to 449, AT3 569 to 924, DH3 950 to 1148, KR3 1412 to 1596, and ACP3 1689 to 1772 in SEQ ID NO:3; KS4 43 to 465, AT4 588 to 916, KR4 1178 to 1356, and ACP4 1451 to 1534 in SEQ ID NO:4; KS5 1556 to 1980, AT5 2095 to 2425, DH5 2451 to 2636, KR5 3274 to 3453, and ACP5 3548 to 3631 in SEQ ID NO:4; KS6 36 to 459, AT6 582 to 910, KR6 1155 to 1335, and ACP6 1421 to 1504 in SEQ ID NO:5; KS7 38 to 461, AT7 581 to 913, KR7 1171 to 1355, ACP7 1443 to 1526, and TE7 1663 to 1695 in SEQ ID NO:6.

Although not wishing to be bound to any particular technical explanation, sequence similarity exists among domain boundaries in various polyketide synthase genes. Thus, one skilled in the art is able to predict the domain boundaries of newly discovered polyketide synthase genes based on the sequence information of known polyketide synthase genes. In particular, the boundaries of submodules, domains, and open reading frames in the instant application are predicted based on sequence information disclosed in the instant application and the locations of the domain boundaries of the erythromycin polyketide synthase (Donadio et al., Gene 111:51 (1992)).

The DNA sequence of the ty lactone synthase gene was determined from recombinant DNA clones prepared from the DNA of *Streptomyces fradiae*. The ty lactone synthase gene is contained in recombinant DNA vectors pSET506 and pSET507 (Figure 3), which are available from the National Center for Agricultural Utilization Research, 1815 North University Street, Peoria, Illinois 61604-3999, in *E. coli* K12 MM294 under accession numbers NRRL B-18688 (deposited July 19, 1990) and NRRL B-18689 (deposited July 19, 1990), respectively.

Techniques for isolating bacterial DNA are readily available and well known in the art. Any such technique can be employed in this invention. In particular, DNA from these cultures is isolated as follows. Lyophilis of *E. coli* K12 MM294/pSET506 or *E. coli* K12 MM294/pSET507 are plated onto L-agar (10 g tryptone, 10 g NaCl, 5 g yeast extract, and 15 g agar per liter) plates containing 100 µg/ml ampicillin to obtain a single colony isolate of the strain. This colony is used to inoculate about 500 ml of L-broth (10 g tryptone, 10 g NaCl, 5 g yeast extract per liter) containing 100 µg/ml ampicillin, and the resulting culture is incubated at 37° C with aeration until the cells reach stationary phase. Cosmid DNA is obtained from the cells in accordance with procedures known in the art (see e.g., Rao et al., 1987 in Methods in Enzymology, 153:166).

DNA of the current invention can be sequenced using any known techniques in the art such as the dideoxynucleotide chain-termination method (Sanger, et al., Proc. Natl. Acad. Sci. 74:5463 (1977)) with either radioisotopic or fluorescent labels. Double-stranded, supercoiled DNA was used directly for templates in sequence reactions with sequence-specific oligonucleotide primers. Alternatively, fragments were used to prepare libraries of either random, overlapping sequences in the bacteriophage M13 or nested, overlapping deletions in a plasmid vector. Individual recombinant DNA subclones were then sequenced with vector-specific oligonucleotide primers. Radioactive reaction products were electrophoresed on denaturing polyacrylamide gels and analyzed by autoradiography. Fluorescent-labeled reaction products were electrophoresed and analyzed on Applied Biosystems (ABI Division, Perkin Elmer, Foster City, CA 94404) model 370A and 373A or DuPont (Wilmington, DE) Genesis DNA sequencers. Sequence data was assembled and edited using Genetic Center Group (GCG, Madison, WI) programs GelAssemble and Seqed or the ABI model 670 Inherit Sequence Analysis system and the AutoAssembler and SeqEd programs.

Polypeptides corresponding to a domain, a synthase unit, or a multi-functional polypeptide can be produced by expression of the cDNA sequence in a bacteria, for example, using known expression vectors. Alternatively, the polypeptides mentioned above can be extracted from ty lactone-producing bacteria such as *Streptomyces fradiae*. In addition, the techniques of synthetic chemistry can be employed to synthesize the polypeptides mentioned above. The procedures and techniques for isolation and purification of homogenous protein or polypeptides are well known in the art.

Since the genetic organization of the ty lactone synthase gene cluster appears to correspond to the order of the reactions required to complete synthesis of ty lactone, knowledge of the ty lactone synthase DNA sequence, its genetic organization, and the activities associated with particular open reading frames, modules, and submodules of the gene enables production of novel polyketides having a predicted structure that are not otherwise available. Modifications may be made to the DNA sequence that either alter the initial carboxylic acid building block used or the building block added at any of the condensation steps. The ty lactone synthase gene may also be modified to alter the actual number of condensation steps done, thereby changing the size of the carbon backbone. Modifications to portions of the DNA sequence that encode the post-condensation processing activities will alter the functional groups appearing at the various condensation sites on the carbon chain backbone.

These modifications can be accomplished by substituting submodules derived from the ty lactone synthase gene and having known activities for corresponding submodules from another polyketide synthase gene having different activities. Submodules from ty lactone synthase may also be combined with submodules from other polyketide synthase genes to effect additional catalytic steps. Accordingly, a DNA molecule wherein at least one submodule from the ty lactone synthase gene has been combined with, or substituted for, submodules from the DNA sequence of other polyketide synthase genes is also provided by the present invention. Further, submodules that are a part of the present invention may be selectively inactivated thereby giving rise to predictable novel polyketide structures.

For example, a submodule encoding a KS' activity, an AT activity, and an ACP activity, all derived from the first open reading frame of the ty lactone synthase gene (ORF1), were exchanged for the corresponding submodule in the platenolide synthase gene (see Example 2). Platenolide is the polyketide backbone of the antibiotic spiramycin.

The submodule from the ty lactone synthase gene encodes a domain that catalyzes the incorporation of a propionate as the initial building block whereas the corresponding submodule of the platenolide synthase gene encodes a domain that catalyzes the incorporation of an acetate building block. When the resulting DNA molecule was placed into a bacterial strain and grown under conditions promoting polyketide synthesis, a hybrid molecule having the structure that would be predicted by incorporation of an additional methyl side-chain at the start of the growing polyketide chain was synthesized, in particular, 16-methyl platenolide.

One skilled in the art is fully familiar with the degeneracy of the genetic code. Consequently, the skilled artisan can modify the specific DNA sequences provided by this disclosure to provide proteins having the same or improved characteristics compared to those polypeptides specifically provided herein. Also, one skilled in the art can modify the DNA sequences to express an identical protein to those provided, albeit expressed at higher levels. Furthermore, one skilled in the art is familiar with means to prepare synthetically, either partially, or in whole, DNA sequences which would be useful in preparing recombinant DNA vectors or coding sequences which are encompassed by the current invention. Additionally, recombinant means for modifying the DNA sequences provided may include for example site-directed deletion or site-directed mutagenesis. These techniques are well known to those skilled in the art and require no further elaboration here. Consequently, as used herein, DNA which is isolated from natural sources, prepared synthetically or semi-synthetically, or which are modified by recombinant DNA methods, are within the scope of the present invention.

Likewise, those skilled in the art will recognize that the polypeptides of the invention may be expressed recombinantly. Alternatively, these polypeptides may be synthesized as well, either in whole or in part, by conventional known non-recombinant techniques; for example, solid-phase synthesis. Thus, the present invention should not be construed as necessarily limited to any specific vector constructions or means for production of the specific polyketide synthase molecules exemplified. These alternate means for preparing the present polypeptides are meant to be encompassed by the present invention.

Many cyclized polyketides undergo glycosylation at one or more sites. Tylosin is a 16-membered cyclic lactone, ty lactone, with three attached sugar residues. The process of converting ty lactone to tylosin is well known in the art. The present invention also provides the information needed to synthesize novel tylosin-related polyketides based on ty lactone. The principles have already been described above. In addition, any product resulting from post-transcriptional or post-translational modification *in vivo* or *in vitro* based on the DNA sequence information disclosed herein are meant to be encompassed by the present invention.

The following examples are provided for exemplification purposes only and are not intended to limit the scope of the invention which has been described in broad terms above.

EXAMPLE 1

The DNA sequence of the *Streptomyces fradiae* ty lactone synthase gene, *tylG*, was obtained by sequencing the inserts of recombinant DNA subclones containing contiguous or overlapping DNA segments, which when considered cumulatively span the entire region of *tylG*. All sequences representing *tylG* are fully contained in the overlapping cosmid subclones pSET506 and pSET507.

In accord with the current invention, the sequence may now be obtained by subcloning and sequencing the DNA fragment designated by *EcoRI* restriction sites at 3.0 and 4.0 kb on the map presented in Figure 3, the fragment bounded

by the *EcoRI* site at 4.0 kb and the *BamHI* site at 7.5 kb, the fragments bounded by *BamHI* sites at 7.5, 12.0, 23.4, 27.3, 34.6, 39.5, and 50.5 kb.

In order to obtain the *tylG* gene on a single DNA fragment, the 31.6 kb DNA fragment bounded by the *EcoRI* site at 3.0 kb and the *BamHI* site at 34.6 kb is isolated from a partial digestion of pSET506 with the restriction enzymes *EcoRI* and *BamHI*. The 15.9 kb DNA fragment bounded by the *BamHI* sites at 34.6 and 50.5 kb is isolated from a partial digestion of pSET507 with the restriction enzyme *BamHI*. The resulting fragments are ligated and cloned in an appropriate recombinant DNA vector. Clones containing the correct orientation of the two ligated fragments are identified by restriction enzyme site mapping.

EXAMPLE 2

Production of a polyketide hybrid of platenolide and tylactone

The lactone rings of the polyketides platenolide and tylactone undergo an identical set of post-condensation processing steps. However, these two polyketides are synthesized by condensation of more than one type of carboxylic acid and the specific building blocks chosen for incorporation in the two pathways differ. The organization of the platenolide gene cluster is shown in Figure 4 along with the accompanying synthetic pathway in Figure 5. The specific carboxylic acid substrates that are used for each condensation reaction and the post-condensation activities of platenolide synthesis are indicated.

The DNA sequence of the *Streptomyces ambofaciens* platenolide synthase (*srmG*) genes was obtained by sequencing inserts of recombinant DNA subclones containing contiguous or overlapping DNA segments, which when considered together span the entire *srmG* region. All sequences representing *srmG* are fully contained in the overlapping cosmid clones pKC1080 and pKC1306 (Figure 6). The sequence can be obtained by subcloning and sequencing the fragments bounded by *NruI* sites at position 1, 0.3 kb, 8.2 kb, 14.1 kb, 20.2 kb, 29.5 kb, 31.4 kb, 41.1 kb, and 42.0 kb.

In order to obtain the *srmG* region on a single fragment, the 25.0 kb fragment bounded by the *NruI* site at position 1 and the *SfuI* site at 25.0 kb is isolated from a partial digestion of pKC1080 with restriction enzymes *NruI* and *SfuI*. The 17.8 kb DNA fragment bounded by the *SfuI* sites at 25.0 kb and 42.8 kb is isolated by digestion of pKC1306 with the restriction enzyme *SfuI*. The resulting fragments are ligated and cloned in an appropriate recombinant DNA vector. Clones containing the correct orientation of the two ligated fragments are identified by restriction enzyme mapping.

An exchange of tylactone polyketide synthase DNA with corresponding platenolide DNA was effected as follows in order to generate a novel polyketide structure.

A strain of *Streptomyces ambofaciens*, the organism that produces platenolide, was constructed with most of ORF1 deleted. This ORF1-deficient strain produced no detectable platenolide. To confirm that the lack of ORF1 was the only deficiency in platenolide production, a construct containing ORF1, and not any functional activities of ORFs 2-5, was introduced into the ORF1-deficient strain on a vector that contains the site-specific integration function from the streptomycete phage ϕ C31. Integration of ORF1 at the ϕ C31 *att* site restored spiramycin production to parental levels, confirming that ORF1 codes for a functional protein and that ORFs 2-5 are expressed in the ORF1-deficient strain.

ORF1 of *tylG* is organized like *srmG* ORF1. DNA coding for a KS', an AT, and an ACP from *tylG* ORF1 was exchanged with the corresponding region from *srmG* ORF1 by replacing an *EcoRI*-*Apal* fragment of *srmG* ORF1 with an *EcoRI*-*SfuI* fragment from *tylG* ORF1, generating plasmid pKC1524. When pKC1524 was introduced into the ORF1-deficient strain, polyketide synthesis was restored. The products produced by this restored strain were indistinguishable from those produced by the parental strain of *Streptomyces ambofaciens* when analyzed by thin-layer chromatography and HPLC.

The hybrid ORF1 DNA sequence is SEQ ID NO:7 and the amino acid sequence of the ORF1-encoded polypeptide is SEQ ID NO:8. The rest of the DNA sequence of the hybrid molecule is identical to original *tylG* sequence and the polypeptides encoded by this remaining portion are therefore identical as well.

In order to simplify physical analysis of the putative novel polyketide, an *XhoI* fragment encoding sugar synthesis or addition was deleted from the restored. Deletion of this fragment led to a strain that produced only the lactone without any sugar residues added. When analyzed by NMR and mass spectroscopy, the isolated product made by this sugar-deficient strain was confirmed as 16-methylplatenolide, which is the structure that would be predicted from the incorporation of a propionate in place of the acetate normally utilized in platenolide synthesis.

SEQUENCE LISTING

5

10

(1) GENERAL INFORMATION:

15

- (i) APPLICANT: ELI LILLY AND COMPANY
- (B) STREET: Lilly Corporate Center
- (C) CITY: Indianapolis
- (D) STATE: Indiana
- (E) COUNTRY: United States of America
- (F) ZIP: 46285

20

(ii) TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES

(iii) NUMBER OF SEQUENCES: 15

25

- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: K. G. TAPPING
- (B) STREET: Erl Wood Manor
- (C) CITY: Windlesham
- (D) STATE: Surrey
- (E) COUNTRY: United Kingdom
- (F) ZIP: GU20 6PH

30

- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: Macintosh
- (C) OPERATING SYSTEM: Macintosh 7.0
- (D) SOFTWARE: Microsoft Word 5.1

35

40

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43280 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

45

(ii) MOLECULE TYPE: DNA (genomic)

50

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 816..14234

55

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 14351..19945

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 20010..31199

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 31232..36067

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 36249..41774

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

15	GAATTCGCGG TCCGCTCGGG TTCCGGTCCG TTTTCTGCTT CGAGCGTCTG TGTCGTCATC	60
	TCGGCTCTCT CATCGGGCTG GTGCGGGAAG GCATCCCGGT GCGGGGAGAC ATCCTGCTGC	120
	GGAAGGAAT CCTGCTCGG GAAGGCAACG ACTGCGGGAC GCGGGAGAAA GGGGAATCGG	180
20	CGGGAATTTT CCCC CGCGG CGGGGACGGT GCCGGAGAAC AACGGCGGGG AAACAGCCCCG	240
	CGGTCCGTGA CGACAACGGA AACTATGGTC CGCTTCTCTC GTCCACAAGG CGGAACCTGA	300
	CATAGTCCCC GCCCAGCGGG AAATCCCGCA CGGCGGCCCG CCGGCCGCCG CACCGGACCT	360
25	GACATAGCCT CGCCGGACCG CTCCGGTGCG GCCACCCCGT TGGTGTGGG TGATGAGGTA	420
	CCGGATCAGA GGAGAAAGCA CCATGCCCCG CCCCTCGGCC AGCGAACCGC GCGGGACCAC	480
30	CCGTTCGGCG ACCCGCGCTG CGCGCCGCCG TGGACCGGC CGTAACTCCC CTGCGCCATC	540
	GAATACTTCG CCCTCGAAT CCCTCACCAG GCGAGTTCCA GGACCGCCCC TCGCTCTCGC	600
	CATACCGGAG AACGAACCG AACGGCACGG CGGAAAGCCC GTCCGCAATG CCGGGACAT	660
35	TCCTGTGACC CGACAACAG GTTTGCGGAC ACGGTTGCC GCAACGCTTG TTGGCAGGCT	720
	CACCGGCACG GCCCGCTGAC ACAGCTCGGT GACACGGCAG CCGTACGGGA AACCGCGGAA	780
40	GCCTCTGGAG TCCTGCGACA TTCGGGAGAG AACAG GTG TCT TCC GCG CTG CGG	833
	Met Ser Ser Ala Leu Arg 1 5	
45	CGC GCG GTG CAA TCC AAC TGT GGC TAC GGA GAC CTC ATG ACC TCG AAC	881
	Arg Ala Val Gln Ser Asn Cys Gly Tyr Gly Asp Leu Met Thr Ser Asn 10 15 20	
50	ACC GCT GCA CAG AAC ACC GGC GAC CAG GAA GAC GTC GAC GGT CCC GAC	929
	Thr Ala Ala Gln Asn Thr Gly Asp Gln Glu Asp Val Asp Gly Pro Asp 25 30 35	
55	AGC ACA CAC GGT GGG GAG ATC GCC GTC GTG GGA ATG TCG TGC CGT CTG	977
	Ser Thr His Gly Gly Glu Ile Ala Val Val Gly Met Ser Cys Arg Leu 40 45 50	
60	CCG GGC GCG GCC GGT GTC GAG GAA TTC TGG GAA CTG CTG CGC AGC GGA	1025
65	Pro Gly Ala Ala Gly Val Glu Glu Phe Trp Glu Leu Leu Arg Ser Gly 55 60 65 70	

	CGC GGT ATG CCC ACC CGT CAG GAC GAC GGC ACC TGG CGG GCC GCC CTG	1073
	Arg Gly Met Pro Thr Arg Gln Asp Asp Gly Thr Trp Arg Ala Ala Leu	
	75 80 85	
5	GAG GAC CAC GCC GGC TTC GAC GCC GGG TTC TTC GGC ATG AAC GCC CGG	1121
	Glu Asp His Ala Gly Phe Asp Ala Gly Phe Phe Gly Met Asn Ala Arg	
	90 95 100	
10	CAG GCC GCC GCC ACC GAC CCG CAG CAC CGA CTG ATG CTG GAA CTC GGA	1169
	Gln Ala Ala Ala Thr Asp Pro Gln His Arg Leu Met Leu Glu Leu Gly	
	105 110 115	
15	TGG GAG GCA CTG GAG GAC GCG GGC ATC GTC CCC GGC GAT CTC ACC GGC	1217
	Trp Glu Ala Leu Glu Asp Ala Gly Ile Val Pro Gly Asp Leu Thr Gly	
	120 125 130	
	ACC GAC ACC GGA GTC TTC GCC GGC GTG GCG TCC GAC GAC TAT GCC GTT	1265
	Thr Asp Thr Gly Val Phe Ala Gly Val Ala Ser Asp Asp Tyr Ala Val	
	135 140 145 150	
20	CTC ACC CGC CGT TCC GCC GTC TCC GCC GGG GGA TAC ACC GCC ACG GGG	1313
	Leu Thr Arg Arg Ser Ala Val Ser Ala Gly Gly Tyr Thr Ala Thr Gly	
	155 160 165	
25	CTG CAC CGC GCC CTG GCC GCC AAC CGC CTC TCC CAC TTC CTG GGC CTG	1361
	Leu His Arg Ala Leu Ala Ala Asn Arg Leu Ser His Phe Leu Gly Leu	
	170 175 180	
	CGC GGC CCC AGC CTG GTC GTC GAC TCG GCC CAG TCC GCC TCA CTG GTG	1409
	Arg Gly Pro Ser Leu Val Val Asp Ser Ala Gln Ser Ala Ser Leu Val	
	185 190 195	
30	GCC GTC CAG CTC GCC TGC GAG AGT CTG CGC CGG GGT GAG ACG TCG CTC	1457
	Ala Val Gln Leu Ala Cys Glu Ser Leu Arg Arg Gly Glu Thr Ser Leu	
	200 205 210	
35	GCC GTC GCG GGC GGT GTC AAC CTC ATC CTC ACC GAG GAG AGC ACC ACC	1505
	Ala Val Ala Gly Gly Val Asn Leu Ile Leu Thr Glu Glu Ser Thr Thr	
	215 220 225 230	
40	GTC ATG GAG CGT ATG GGA GCG CTC TCA CCC GAC GGC CGC TGC CAC ACC	1553
	Val Met Glu Arg Met Gly Ala Leu Ser Pro Asp Gly Arg Cys His Thr	
	235 240 245	
45	TTC GAC GCC CGC GCC AAC GGC TAC GTA CGC GGC GAG GGC GGC GGA GCC	1601
	Phe Asp Ala Arg Ala Asn Gly Tyr Val Arg Gly Glu Gly Gly Gly Ala	
	250 255 260	
	GTC GTG CTC AAG CCA CTG GAC GCC GCA CTC GCC GAC GGC GAC CGC GTG	1649
	Val Val Leu Lys Pro Leu Asp Ala Ala Leu Ala Asp Gly Asp Arg Val	
	265 270 275	
50	TAC TGC GTC ATC AAG GGA GGT GCC GTC AAC AAC GAC GGC GGC GGC GCG	1697
	Tyr Cys Val Ile Lys Gly Gly Ala Val Asn Asn Asp Gly Gly Gly Ala	
	280 285 290	
55	AGC CTC ACC ACT CCC GAC CGG GAG GCG CAG GAA GCT GTG CTG CGC CAG	1745
	Ser Leu Thr Thr Pro Asp Arg Glu Ala Gln Glu Ala Val Leu Arg Gln	
	295 300 305 310	

	GCC TAC CGG CGG GCG GGC GTC AGC ACC GGC GCC GTC CGC TAC GTC GAG	1793
	Ala Tyr Arg Arg Ala Gly Val Ser Thr Gly Ala Val Arg Tyr Val Glu	
	315 320 325	
5	CTG CAC GGG ACC GGC ACC CGG GCC GGC GAC CCC GTC GAG GCG GCC GCA	1841
	Leu His Gly Thr Gly Thr Arg Ala Gly Asp Pro Val Glu Ala Ala Ala	
	330 335 340	
10	CTG GGC GCC GTG CTC GGG GCG GGG GCG GAC AGC GGC CGC AGC ACG CCG	1889
	Leu Gly Ala Val Leu Gly Ala Gly Ala Asp Ser Gly Arg Ser Thr Pro	
	345 350 355	
	CTC GCC GTC GGC TCG GTG AAG ACC AAC GTC GGC CAT CTG GAG GGC GCG	1937
15	Leu Ala Val Gly Ser Val Lys Thr Asn Val Gly His Leu Glu Gly Ala	
	360 365 370	
	GCG GGC ATC GTC GGA CTG ATC AAG GCC ACG CTG TGC GTA CCG AAG GGC	1985
	Ala Gly Ile Val Gly Leu Ile Lys Ala Thr Leu Cys Val Arg Lys Gly	
	375 380 385 390	
20	GAA CTC GTC CCC AGC CTC AAC TTC AGC ACG CCG AAC CCT GAC ATC CCC	2033
	Glu Leu Val Pro Ser Leu Asn Phe Ser Thr Pro Asn Pro Asp Ile Pro	
	395 400 405	
25	CTC GAC GAC CTG CGG CTG CCG GTC CAG ACC GAA CCG CAG GAG TGG AAC	2081
	Leu Asp Asp Leu Arg Leu Arg Val Gln Thr Glu Arg Gln Glu Trp Asn	
	410 415 420	
	GAG GAG GAC GAC CCG CCG CCG GTG GCC GGC GTC TCC TCC TTC GGT ATG	2129
30	Glu Glu Asp Asp Arg Pro Arg Val Ala Gly Val Ser Ser Phe Gly Met	
	425 430 435	
	GGC GGA ACC AAT GTC CAC CTC GTG ATC GCG GAG GCT CCG GCC GCG GCG	2177
	Gly Gly Thr Asn Val His Leu Val Ile Ala Glu Ala Pro Ala Ala Ala	
	440 445 450	
35	GGG TCC TCC GGG GCG GCG GGT TCG GGC GCT GGT TCC GGT GCC GGT ATC	2225
	Gly Ser Ser Gly Ala Gly Gly Ser Gly Ala Gly Ser Gly Ala Gly Ile	
	455 460 465 470	
	AGC GCT GTT TCT GGT GTG GTG CCG GTG GTG GTT TCG GCG CGT TCG CCG	2273
40	Ser Ala Val Ser Gly Val Val Pro Val Val Val Ser Gly Arg Ser Arg	
	475 480 485	
	GTG GTG GTG CCG GAG GCT CCG GGC CCG TTG GCG GAG GTG GTG GAG GCC	2321
45	Val Val Val Arg Glu Ala Ala Gly Arg Leu Ala Glu Val Val Glu Ala	
	490 495 500	
	GGT GGT GTG GGG CTG GCG GAT GTG GCG GTG ACG ATG GCG GAC CCG TCG	2369
	Gly Gly Val Gly Leu Ala Asp Val Ala Val Thr Met Ala Asp Arg Ser	
	505 510 515	
50	CGG TTT GGG TAT CGG GCG GTT GTG CTG GCT CCG GGT GAG GCT GAG CTT	2417
	Arg Phe Gly Tyr Arg Ala Val Val Leu Ala Arg Gly Glu Ala Glu Leu	
	520 525 530	
55	GCC GGG CGT TTG CCG GCG TTG GCG GGG GGT GAT CCG GAC GCG GGT GTG	2465
	Ala Gly Arg Leu Arg Ala Leu Ala Gly Gly Asp Pro Asp Ala Gly Val	
	535 540 545 550	

	GTC ACC GGT GCG GTT CTC GAC GGT GGT GTG GTT GTC GGT GCT GCC CCC	2513
	Val Thr Gly Ala Val Leu Asp Gly Gly Val Val Val Gly Ala Ala Pro	
	555 560 565	
5	GGC GGT GCC GGT GCT GCC GGT GGT GCC GGT GCT GCC GGT GGT GCC GGT	2561
	Gly Gly Ala Gly Ala Ala Gly Gly Ala Gly Ala Ala Gly Gly Ala Gly	
	570 575 580	
10	GGT GGG GGC GTG GTG TTG GTT TTC CCT GGT CAG GGG ACG CAG TGG GTG	2609
	Gly Gly Gly Val Val Leu Val Phe Pro Gly Gln Gly Thr Gln Trp Val	
	585 590 595	
	GGG ATG GGT GCG GGG CTG CTG GGG TCT TCG GAG GTG TTT GCG GCG TCG	2657
15	Gly Met Gly Ala Gly Leu Leu Gly Ser Ser Glu Val Phe Ala Ala Ser	
	600 605 610	
	ATC CGG GAG TGT GCG CCG GCG CTG AGT GTT CAT GTG GGG TCG GAT TTG	2705
	Met Arg Glu Cys Ala Arg Ala Leu Ser Val His Val Gly Trp Asp Leu	
	615 620 625 630	
20	CTG GAG GTG GTG TCG GCG GGG GCC GGG TTG GAG CCG GTG GAT GTG GTG	2753
	Leu Glu Val Val Ser Gly Gly Ala Gly Leu Glu Arg Val Asp Val Val	
	635 640 645	
	CAG CCG GTG ACG TGG GCG GTG ATG GTG TCG CTG GCC CCG TAC TGG CAG	2801
25	Gln Pro Val Thr Trp Ala Val Met Val Ser Leu Ala Arg Tyr Trp Gln	
	650 655 660	
	GCG ATG GGT GTG GAC GTG GCT GCG GTG GTG GGT CAT TCC CAG GCG GAG	2849
30	Ala Met Gly Val Asp Val Ala Ala Val Val Gly His Ser Gln Gly Glu	
	665 670 675	
	ATC GCC GCT GCC ACG GTG GCG GGG GCG TTG TCG CTG GAG GAT GCG GCG	2897
	Ile Ala Ala Ala Thr Val Ala Gly Ala Leu Ser Leu Glu Asp Ala Ala	
	680 685 690	
35	GCT GTG GTC GCT CTG CCG GCG GGG TTG ATT GGC CCG TAT CTG GCG GGT	2945
	Ala Val Val Ala Leu Arg Ala Gly Leu Ile Gly Arg Tyr Leu Ala Gly	
	695 700 705 710	
	CGT GGT GCG ATG GCG GCT GTT CCG CTG CCT CCC GCG GAG GTC GAG GCC	2993
40	Arg Gly Ala Met Ala Ala Val Pro Leu Pro Ala Gly Glu Val Glu Ala	
	715 720 725	
	GGG CTG GCG AAG TGG CCG GGT GTG GAG GTC GCG GCG GTC AAC GGT CCG	3041
45	Gly Leu Ala Lys Trp Pro Gly Val Glu Val Ala Ala Val Asn Gly Pro	
	730 735 740	
	GCG TCT ACG GTG GTT TCC GCG GAT CCG CCG GCG GTG GCC GGT TAT GTG	3089
	Ala Ser Thr Val Val Ser Gly Asp Arg Arg Ala Val Ala Gly Tyr Val	
	745 750 755	
50	GCC GTC TGT CAG GCG GAG GGT GTG CAG GCC CCG TTG ATA CCG GTG GAC	3137
	Ala Val Cys Gln Ala Glu Gly Val Gln Ala Arg Leu Ile Pro Val Asp	
	760 765 770	
55	TAC GCC TCT CAC TCC CCG CAT GTG GAG GAC CTG AAG GCG GAG TTG GAG	3185
	Tyr Ala Ser His Ser Arg His Val Glu Asp Leu Lys Gly Glu Leu Glu	
	775 780 785 790	

	CGG GTG CTG TCC GGT ATC CGC CCC CGC AGT CCG CGG GTG CCG GTG TGT	3233
	Arg Val Leu Ser Gly Ile Arg Pro Arg Ser Pro Arg Val Pro Val Cys	
	795 800 805	
5	TCC ACC GTC GCC GGA GAG CAG CCG GGC GAG CCG GTT TTC GAT GCG GGG	3281
	Ser Thr Val Ala Gly Glu Gln Pro Gly Glu Pro Val Phe Asp Ala Gly	
	810 815 820	
10	TAT TGG TTC CGT AAT CTG CGG AAC CCG GTT GAG TTC TCC GCG GTG GTC	3329
	Tyr Trp Phe Arg Asn Leu Arg Asn Arg Val Glu Phe Ser Ala Val Val	
	825 830 835	
15	GGT GGT TTG TTG GAG GAG GGC CAC CGT CCG TTC ATC GAG GTC AGT GCC	3377
	Gly Gly Leu Leu Glu Glu Gly His Arg Arg Phe Ile Glu Val Ser Ala	
	840 845 850	
	CAC CCG GTA CTC GTC CAT GCG ATC GAG CAG ACG GCC GAG GCC GCG GAC	3425
	His Pro Val Leu Val His Ala Ile Glu Gln Thr Ala Glu Ala Ala Asp	
	855 860 865 870	
20	CGG AGT GTC CAT GCC ACC GGG ACC CTG CCG CCG CAG GAC GAC AGC CCG	3473
	Arg Ser Val His Ala Thr Gly Thr Leu Arg Arg Gln Asp Asp Ser Pro	
	875 880 885	
25	CAC CCG CTG CTG ACC TCC ACC GCC GAG GCC TGG GCC CAC GGC GCC ACC	3521
	His Arg Leu Leu Thr Ser Thr Ala Glu Ala Trp Ala His Gly Ala Thr	
	890 895 900	
30	CTC ACC TGG GAC CCC GCC CTG CCC CCA GGC CAC CTC ACC ACC CTC CCC	3569
	Leu Thr Trp Asp Pro Ala Leu Pro Pro Gly His Leu Thr Thr Leu Pro	
	905 910 915	
	ACC TAC CCC TTC AAC CAC CAC CAC TAC TGG CTC GAC ACC ATT GAC GGG	3617
	Thr Tyr Pro Phe Asn His His His Tyr Trp Leu Asp Thr Ile Asp Gly	
	920 925 930	
35	GGC GGA GGG GAC GAC GCG ACC CAG GAG AAG GAG AGC GGC CCT CTG ACG	3665
	Gly Gly Gly Asp Asp Ala Thr Gln Glu Lys Glu Ser Gly Pro Leu Thr	
	935 940 945 950	
40	CGG GAA CTG CGT GGG CTG CCG TCC TCT CAG AAG CAA CTG GGT TTC CTG	3713
	Arg Glu Leu Arg Gly Leu Pro Ser Ser Gln Lys Gln Leu Gly Phe Leu	
	955 960 965	
	CTC GAT CTG GTG TGC CGG CAC ACG GCC GTC GTA CTC GGC CTG GAC ACG	3761
	Leu Asp Leu Val Cys Arg His Thr Ala Val Val Leu Gly Leu Asp Thr	
	970 975 980	
45	GCC GCC GAG GTG GAC CCG GAC CTG TCC TTC AAG AAG CAG GGC ATC CAG	3809
	Ala Ala Glu Val Asp Pro Asp Leu Ser Phe Lys Lys Gln Gly Ile Gln	
	985 990 995	
50	TCC ATG ACC GGC GTC GAG CTG CGC AAC AGG CTG CTG ACC GAG ACC GGC	3857
	Ser Met Thr Gly Val Glu Leu Arg Asn Arg Leu Leu Thr Glu Thr Gly	
	1000 1005 1010	
55	CTG GCA TTG CCC ACC ACC CTC GTC TAC GAC CCG CCC ACC CCT CGC GCC	3905
	Leu Ala Leu Pro Thr Thr Leu Val Tyr Asp Arg Pro Thr Pro Arg Ala	
	1015 1020 1025 1030	

	CTG GCG CAG TTC CTC CAC ACC GAG TTG CTC GAC GGC TCC CCC TCG GGC	3953
	Leu Ala Gln Phe Leu His Thr Glu Leu Leu Asp Gly Ser Pro Ser Gly	
	1035 1040 1045	
5	TCC GTC CTC GCA CCG GCG CAG AAG AGC TTC GAA GCC CAG GAG CCG ATC	4001
	Ser Val Leu Ala Pro Ala Gln Lys Ser Phe Glu Ala Gln Glu Pro Ile	
	1050 1055 1060	
10	GCG GTC CTG GGT ATG GGG TGC CCG TTC CCC GGT GGG GTG GGT TCG CCG	4049
	Ala Val Val Gly Met Gly Cys Arg Phe Pro Gly Gly Val Gly Ser Pro	
	1065 1070 1075	
	GAG GCG TTG TGG CCG TTG GTG GTG GAG GGG GTG GAC GCG GTT TCC CCG	4097
	Glu Ala Leu Trp Arg Leu Val Val Glu Gly Val Asp Ala Val Ser Pro	
15	1080 1085 1090	
	TTT CCC GGT GAT CGT GGC TGG GAT GTG GAG GGG TTG TAC GAC CCG GAG	4145
	Phe Pro Gly Asp Arg Gly Trp Asp Val Glu Gly Leu Tyr Asp Pro Glu	
	1095 1100 1105 1110	
20	CCG GGT GTG GCG GGG AAG TCG TAT GTG CCG GAG GGG GGT TTT CTG CAT	4193
	Pro Gly Val Ala Gly Lys Ser Tyr Val Arg Glu Gly Gly Phe Leu His	
	1115 1120 1125	
25	GAT GCG GCG GAG TTC GAT GCG GAG TTC TTC GGG ATT TCG CCG CGT GAG	4241
	Asp Ala Ala Glu Phe Asp Ala Glu Phe Phe Gly Ile Ser Pro Arg Glu	
	1130 1135 1140	
	GCG GTG GCG ATG GAT CCG CAG CAG CCG CTG TTG CTG GAG ACC TCC TCG	4289
	Ala Val Ala Met Asp Pro Gln Gln Arg Leu Leu Leu Glu Thr Ser Trp	
30	1145 1150 1155	
	GAG GCG ATC GAG CCG GCG GGT ATC GAC CCG CAC TCG CTG CAC GGC AGC	4337
	Glu Ala Ile Glu Arg Ala Gly Ile Asp Pro His Ser Leu His Gly Ser	
	1160 1165 1170	
35	CGC ACC GGC GTC TAC GCC GGC GTG ATG CCG CAG GAA TAC GGA CCT CCG	4385
	Arg Thr Gly Val Tyr Ala Gly Val Met Pro Gln Glu Tyr Gly Pro Arg	
	1175 1180 1185 1190	
	CTC GCC GAA GGA GCG GAA GGC AGC GAC GGC TAC CTC CTC ACC GGT ACG	4433
	Leu Ala Glu Gly Ala Glu Gly Ser Asp Gly Tyr Leu Leu Thr Gly Thr	
40	1195 1200 1205	
	TCG GGG AGT GTG GTG TCG GGG CGT GTG GCC TAC ACG CTG GGG CTG GAG	4481
	Ser Gly Ser Val Val Ser Gly Arg Val Ala Tyr Thr Leu Gly Leu Glu	
45	1210 1215 1220	
	GGT CCG GCC GTG ACC GTG GAT ACG GCG TGT TCG TCG TCG TTG GTG GCG	4529
	Gly Pro Ala Val Thr Val Asp Thr Ala Cys Ser Ser Ser Leu Val Ala	
	1225 1230 1235	
50	TTG CAT CTG GCG GTG CAG GCG TTG CCG GGT GGC GAG TGT GAC ATG GCG	4577
	Leu His Leu Ala Val Gln Ala Leu Arg Gly Gly Glu Cys Asp Met Ala	
	1240 1245 1250	
55	TTG GCC GGT GGT GTG ACG GTG ATG GCC GGG CCG GGG ATG TTC GTG GAG	4625
	Leu Ala Gly Gly Val Thr Val Met Ala Gly Pro Gly Met Phe Val Glu	
	1255 1260 1265 1270	

	TTT TCG CCG CAG CCG GCG TTG GCG GCC GAT GGG CCG TGC AAG GCG TTC	4673
	Phe Ser Arg Gln Arg Gly Leu Ala Ala Asp Gly Arg Cys Lys Ala Phe	
	1275 1280 1285	
5	CGG GAT GGG GCG GAT GGG ACC GCT TGG GCC GAG GGT CCG GGG GTG GTG	4721
	Ala Asp Gly Ala Asp Gly Thr Ala Trp Ala Glu Gly Ala Gly Val Val	
	1290 1295 1300	
10	CTG GTG GAG CCG TTG TCG GAT GCC CCG CCG TTG GGG CAT CCG GTG TTG	4769
	Leu Val Glu Arg Leu Ser Asp Ala Arg Arg Leu Gly His Pro Val Leu	
	1305 1310 1315	
	GCG GTG GTG TGT GGG TCG GCG GTG AAT CAG GAC GGT GCG TCG AAT GGT	4817
	Ala Val Val Cys Gly Ser Ala Val Asn Gln Asp Gly Ala Ser Asn Gly	
15	1320 1325 1330	
	TTG ACG GCG CCG AGT GGT CCG TCG CAG GAG CCG GTG ATT CGT CAG GCC	4865
	Leu Thr Ala Pro Ser Gly Pro Ser Gln Glu Arg Val Ile Arg Gln Ala	
	1335 1340 1345 1350	
20	TTG GGG AAT GCG CCG TTG ACG GTG GCG GAT GTG GAT GTG GTG GAG GCG	4913
	Leu Gly Asn Ala Arg Leu Thr Val Ala Asp Val Asp Val Val Glu Ala	
	1355 1360 1365	
25	CAT GGG ACG GGG ACG CCG CTG GGT GAT CCG ATC GAG GCG CAG GCG TTG	4961
	His Gly Thr Gly Thr Arg Leu Gly Asp Pro Ile Glu Ala Gln Ala Leu	
	1370 1375 1380	
	CTG GGG ACG TAT GGG CCG GAT CGT GAT GGT GGG CGT CCG GTG TGG TTG	5009
	Leu Gly Thr Tyr Gly Arg Asp Arg Asp Gly Gly Arg Pro Val Trp Leu	
30	1385 1390 1395	
	GGG TCG TTG AAG TCG AAT ATT GGT CAT GCT CAG GCG GCT GCG GGG GTG	5057
	Gly Ser Leu Lys Ser Asn Ile Gly His Ala Gln Ala Ala Ala Gly Val	
	1400 1405 1410	
35	GCT GGT GTG ATC AAG ATG GTG TTG GCG ATG CCG TAT GGG TGG TTG CCG	5105
	Ala Gly Val Ile Lys Met Val Leu Ala Met Arg Tyr Gly Trp Leu Pro	
	1415 1420 1425 1430	
	CGG ACG TTG CAT GTG GAT GAG CCG AGC CCG CAT GTG GAC TGG TCG GCT	5153
	Arg Thr Leu His Val Asp Glu Pro Ser Arg His Val Asp Trp Ser Ala	
40	1435 1440 1445	
	GGT GGT GTG TGG TTG CTG ACC GAG GCG CCG GAG TGG CCG GGG GTG GAC	5201
	Gly Gly Val Trp Leu Leu Thr Glu Ala Arg Glu Trp Pro Gly Val Asp	
45	1450 1455 1460	
	CGG CCG CGT CCG GCG GCG GTC TCC GCC TTT GGT GTC AGT GGT ACC AAC	5249
	Arg Pro Arg Arg Ala Ala Val Ser Ala Phe Gly Val Ser Gly Thr Asn	
	1465 1470 1475	
50	GCC CAT CTG ATC CTC GAA GCC CCC GAC ACC GCC GAG GCG GAG AGC GCC	5297
	Ala His Leu Ile Leu Glu Ala Pro Asp Thr Ala Glu Ala Glu Ser Ala	
	1480 1485 1490	
55	ACG ACC CCG GTC CCG TCT GAG GTG TCG GAG TCT GCT GCG GTC CTC GAT	5345
	Thr Thr Pro Val Arg Ser Glu Val Ser Glu Ser Ala Ala Val Leu Asp	
	1495 1500 1505 1510	

	GCC CGC AGT GGT GTG GTG CCG GTG GTG GTT TCG GGC CGT TCG CGG GTG	5393
	Ala Arg Ser Gly Val Val Pro Val Val Val Ser Gly Arg Ser Arg Val	
	1515 1520 1525	
5	GTG GTG CCG GAG GCT GCG GGC CCG TTG GCG GAG GTG GTG GAG GCC GGT	5441
	Val Val Arg Glu Ala Ala Gly Arg Leu Ala Glu Val Val Glu Ala Gly	
	1530 1535 1540	
10	GGT GTG GGC CTG GCG GAT GTG GCG GTG ACG ATG GCG GGC CCG TCG CGG	5489
	Gly Val Gly Leu Ala Asp Val Ala Val Thr Met Ala Gly Arg Ser Arg	
	1545 1550 1555	
15	TTT GGG TAT CCG GCG GTT GTG CTG GCT CCG GGT GAG GCT GAG CTT GCC	5537
	Phe Gly Tyr Arg Ala Val Val Leu Ala Arg Gly Glu Ala Glu Leu Ala	
	1560 1565 1570	
	GGG CGT TTG CCG GCG TTG GCG GGC GGT GAT CCG GAC GCG GGT GTG GTC	5585
	Gly Arg Leu Arg Ala Leu Ala Gly Gly Asp Pro Asp Ala Gly Val Val	
	1575 1580 1585 1590	
20	ACC GGT GCG GTG GTG GAC CCG GAG ACG GCG TCC GGT GGT GCG GGC GTG	5633
	Thr Gly Ala Val Val Asp Pro Glu Thr Gly Ser Gly Gly Gly Gly Val	
	1595 1600 1605	
25	GTG TTG GTT TTC CCT GGT CAG GGG ACG CAG TGG GTG GGG ATG GGT GCG	5681
	Val Leu Val Phe Pro Gly Gln Gly Thr Gln Trp Val Gly Met Gly Ala	
	1610 1615 1620	
	GGG CTG CTG GCG TCT TCG GAG GTG TTT GCG GCG TCG ATG CCG GAG TGT	5729
	Gly Leu Leu Gly Ser Ser Glu Val Phe Ala Ala Ser Met Arg Glu Cys	
30	1625 1630 1635	
	GCG CCG GCG CTG AGT GTT CAT GTG GAG TGG GAT TTG CTG GAG GTG GTG	5777
	Ala Arg Ala Leu Ser Val His Val Glu Trp Asp Leu Leu Glu Val Val	
	1640 1645 1650	
35	TCG GCG GCG GCC GCG TTG GAG CCG GTG GAT GTG GTG CAG CCC GTG ACG	5825
	Ser Gly Gly Ala Gly Leu Glu Arg Val Asp Val Val Gln Pro Val Thr	
	1655 1660 1665 1670	
40	TGG GCG GTG ATG GTG TCG CTG GCC CCG TAC TGG CAG GCG ATG GGT GTG	5873
	Trp Ala Val Met Val Ser Leu Ala Arg Tyr Trp Gln Ala Met Gly Val	
	1675 1680 1685	
	GAC GTG GCT GCG GTG GTG GGT CAT TCC CAG GCG GAG ATC GCT GCT GCC	5921
	Asp Val Ala Ala Val Val Gly His Ser Gln Gly Glu Ile Ala Ala Ala	
45	1690 1695 1700	
	ACG GTG CCG GCG GCG TTG TCG CTG GAG GAT GCG GCG GCT GTG GTC GCT	5969
	Thr Val Ala Gly Ala Leu Ser Leu Glu Asp Ala Ala Val Val Ala	
	1705 1710 1715	
50	CTG CCG GCG GCG TTG ATT GCG CCG TAT CTG GCG GGT CGT GGT GCG ATG	6017
	Leu Arg Ala Gly Leu Ile Gly Arg Tyr Leu Ala Gly Arg Gly Ala Met	
	1720 1725 1730	
55	GCG GCT GTT CCG CTG CCT GCC GCG GAG GTC GAG GCC GCG CTG GCG AAG	6065
	Ala Ala Val Pro Leu Pro Ala Gly Glu Val Glu Ala Gly Leu Ala Lys	
	1735 1740 1745 1750	

	TGG CCG GGT GTG GAG GTC GCG GCG GTC AAC GGT CCG GCG TCC ACG GTG	6113
	Trp Pro Gly Val Glu Val Ala Ala Val Asn Gly Pro Ala Ser Thr Val	
	1755 1760 1765	
5	GTT TCC GGG GAT CCG CCG GCG GTG GCC GGT TAT GTG GCC GTC TGT CAG	6161
	Val Ser Gly Asp Arg Arg Ala Val Ala Gly Tyr Val Ala Val Cys Gln	
	1770 1775 1780	
10	GCG GAG GGT GTG CAG GCT CCG TTG ATA CCG GTG GAC TAC CCC TCT CAC	6209
	Ala Glu Gly Val Gln Ala Arg Leu Ile Pro Val Asp Tyr Ala Ser His	
	1785 1790 1795	
15	TCC CGC CAT GTG GAG GAC CTG AAG GGC GAG TTG GAG CCG GTG CTG TCC	6257
	Ser Arg His Val Glu Asp Leu Lys Gly Glu Leu Glu Arg Val Leu Ser	
	1800 1805 1810	
	GGT ATC CCG CCC CCG AGT CCG CCG GTG CCG GTG TGT TCC ACC GTC GCC	6305
	Gly Ile Arg Pro Arg Ser Pro Arg Val Pro Val Cys Ser Thr Val Ala	
	1815 1820 1825 1830	
20	GGA GAG CAG CCG GGC GAG CCG GTT TTC GAT GCG GGG TAT TGG TTC CGT	6353
	Gly Glu Gln Pro Gly Glu Pro Val Phe Asp Ala Gly Tyr Trp Phe Arg	
	1835 1840 1845	
25	AAT CTG CCG AAC CCG GTT GAG TTC TCC GCG GTG GTC GGT GGT TTG TTG	6401
	Asn Leu Arg Asn Arg Val Glu Phe Ser Ala Val Val Gly Gly Leu Leu	
	1850 1855 1860	
	GAG GAG GGC CAC CGT CCG TTC ATC GAG GTC AGT GCC CAC CCG GTA CTC	6449
	Glu Glu Gly His Arg Arg Phe Ile Glu Val Ser Ala His Pro Val Leu	
30	1865 1870 1875	
	GTC CAT GCG ATC GAG CAG ACG GCC GAG GCC CCG GAC CCG AGT GTC CAT	6497
	Val His Ala Ile Glu Gln Thr Ala Glu Ala Ala Asp Arg Ser Val His	
	1880 1885 1890	
35	GCC ACC GGG ACC CTG CCG CCG CAG GAC GAC AGC CCG CAC CCG CTG CTG	6545
	Ala Thr Gly Thr Leu Arg Arg Gln Asp Asp Ser Pro His Arg Leu Leu	
	1895 1900 1905 1910	
	ACC TCC ACC GCC GAG GCC TGG GCC CAC GGC GCC ACC CTC ACC TGG GAC	6593
40	Thr Ser Thr Ala Glu Ala Trp Ala His Gly Ala Thr Leu Thr Trp Asp	
	1915 1920 1925	
	CCC GCC CTG CCC CCA GGC CAC CTC ACC ACC CTC CCC ACC TAC CCC TTC	6641
	Pro Ala Leu Pro Pro Gly His Leu Thr Thr Leu Pro Thr Tyr Pro Phe	
45	1930 1935 1940	
	AAC CAC CAC CAC TAC TGG CTC GAC ACC ACC CCC ACC ACC CCC GCG ACG	6689
	Asn His His His Tyr Trp Leu Asp Thr Thr Pro Thr Thr Pro Ala Thr	
	1945 1950 1955	
50	ACC ACC CAG AGC CCC ACC GAT GCC TGG CCG TAC CCG GTC ACC TGG AAA	6737
	Thr Thr Gln Ser Pro Thr Asp Ala Trp Arg Tyr Arg Val Thr Trp Lys	
	1960 1965 1970	
55	GCC CTG ACC GAA TCC TCC CCC GTC CCG CCT CAC TCC ATC GGT CCG TGC	6785
	Ala Leu Thr Glu Ser Ser Pro Val Arg Pro His Ser Ile Gly Arg Cys	
	1975 1980 1985 1990	

5	CTC CTC GTT GCA CCC CCG ACC ACC GAC GGC GAG CTC CTC GAC GGA CTG Leu Leu Val Ala Pro Pro Thr Thr Asp Gly Glu Leu Leu Asp Gly Leu 1995 2000 2005	6833
10	ACA ACG GTG TTG TCC GAG CGC GGT GCC TCC GTC GCC CGC CTT GAG GTG Thr Thr Val Leu Ser Glu Arg Gly Ala Ser Val Ala Arg Leu Glu Val 2010 2015 2020	6881
15	CCC ATC GGC GCG CCG CGT GCC GAG GTC GCC GAA CTG CTC AAG CCC TCC Pro Ile Gly Ala Arg Arg Ala Glu Val Ala Glu Leu Leu Lys Pro Ser 2025 2030 2035	6929
20	ATG GAG TCA GCG GGG GAG GAG AAC ACC ACC GTC GTC TCG CTT CTC GGT Met Glu Ser Ala Gly Glu Glu Asn Thr Thr Val Val Ser Leu Leu Gly 2040 2045 2050	6977
25	CTG GTG CCC TCC ACG GAC GCG GTC AGG ACG TCG ATA GCG CTC CTC CAG Leu Val Pro Ser Thr Asp Ala Val Arg Thr Ser Ile Ala Leu Leu Gln 2055 2060 2065 2070	7025
30	GCG GTC TCC GAC ATC GGC GTC CCG GCC GCC AGG GTC TGG GCG CTG ACG Ala Val Ser Asp Ile Gly Val Pro Ala Ala Arg Val Trp Ala Leu Thr 2075 2080 2085	7073
35	CGG AGG GCC GTG GCC GTG GTT CCC GGG GAG ACG CCG CAG GAC GCG GGG Arg Arg Ala Val Ala Val Val Pro Gly Glu Thr Pro Gln Asp Ala Gly 2090 2095 2100	7121
40	GCC CAG TTG TGG GGC TTC GGA CGA GTG GCG GCC CTT GAA CTC CCG GAT Ala Gln Leu Trp Gly Phe Gly Arg Val Ala Ala Leu Glu Leu Pro Asp 2105 2110 2115	7169
45	ATC TGG GGC GGC TTG ATC GAT CTG CCG GAG ACA GCG GAG CTG ACG CCG Ile Trp Gly Gly Leu Ile Asp Leu Pro Glu Thr Ala Glu Leu Thr Arg 2120 2125 2130	7217
50	ACG CCG GAG ACC TCA CAG CCC CCA CAG ACC CCG GAG AGG CTG CCG CAG Thr Pro Glu Thr Ser Gln Pro Pro Gln Thr Pro Glu Arg Leu Pro Gln 2135 2140 2145 2150	7265
55	ACT CCG AAC CGA CGC GCC CTT GAG CTT GCT GCC GCC GTC CTC GCC GGC Thr Pro Asn Arg Arg Ala Leu Glu Leu Ala Ala Val Leu Ala Gly 2155 2160 2165	7313
60	GCG GAC GGC GAG GAC CAG GTC GCC GTG CGC GCC TCG GGG ATC TAC GGG Arg Asp Gly Glu Asp Gln Val Ala Val Arg Ala Ser Gly Ile Tyr Gly 2170 2175 2180	7361
65	CGG CGG GTG TCG CCG GCC GCG GCA GCG GGG GCC GCC TCC TGG CAG CCG Arg Arg Val Ser Arg Ala Ala Ala Glu Ala Ala Ser Trp Gln Pro 2185 2190 2195	7409
70	TCC GGC ACG GTG CTG ATC ACC GGC GGC ATG GGT GCC ATC GGC AGG CCG Ser Gly Thr Val Leu Ile Thr Gly Gly Met Gly Ala Ile Gly Arg Arg 2200 2205 2210	7457
75	CTC GCC CGC AGG CTG GCG GCC GAG GGA GCC GAA CGC CTG GTC CTC ACC Leu Ala Arg Arg Leu Ala Ala Glu Gly Ala Glu Arg Leu Val Leu Thr 2215 2220 2225 2230	7505

	AGC CGT CGC GGA CCG GAG GCG CCG GGC GCC GCC GAA CTC GCC GAG GAA	7553
	Ser Arg Arg Gly Pro Glu Ala Pro Gly Ala Ala Glu Leu Ala Glu Glu	
	2235 2240 2245	
5	CTG CGA GGA CAT GGC TGC GAG GTC GTG CAC GCG GCC TGT GAC GTG GCC	7601
	Leu Arg Gly His Gly Cys Glu Val Val His Ala Ala Cys Asp Val Ala	
	2250 2255 2260	
10	GAG CGT GAT GCG CTC GCC GCG CTC GTC ACC GCG TAT CCG CCG AAC GCC	7649
	Glu Arg Asp Ala Leu Ala Ala Leu Val Thr Ala Tyr Pro Pro Asn Ala	
	2265 2270 2275	
	GTC TTC CAC ACC GCC GGG ATT CTG GAC GAC GCG GTG ATC GAC ACG CTG	7697
	Val Phe His Thr Ala Gly Ile Leu Asp Asp Ala Val Ile Asp Thr Leu	
15	2280 2285 2290	
	TCA CCG GAG AGC TTC GAG ACC GTC CCG GGG GCG AAG GTG TGC GGC GCG	7745
	Ser Pro Glu Ser Phe Glu Thr Val Arg Gly Ala Lys Val Cys Gly Ala	
	2295 2300 2305 2310	
20	GAG CTG CTG CAC CAA CTG ACT GCG GAC ATA AAA GGG TTG GAC GCC TTC	7793
	Glu Leu Leu His Gln Leu Thr Ala Asp Ile Lys Gly Leu Asp Ala Phe	
	2315 2320 2325	
25	GTC CTC TTC TCC TCC GTC ACC GGC ACA TGG GGC AAC GCC GGC CAG GGT	7841
	Val Leu Phe Ser Ser Val Thr Gly Thr Trp Gly Asn Ala Gly Gln Gly	
	2330 2335 2340	
	GCG TAC GCC GCC GCC AAC GCC GCG CTC GAC GCC CTC GCC GAG CGT CGC	7889
	Ala Tyr Ala Ala Ala Asn Ala Ala Leu Asp Ala Leu Ala Glu Arg Arg	
30	2345 2350 2355	
	CGT GCC GCC GGA CTG CCC GCG ACC TCC GTC GCC TGG GGC CTT TGG GGC	7937
	Arg Ala Ala Gly Leu Pro Ala Thr Ser Val Ala Trp Gly Leu Trp Gly	
	2360 2365 2370	
35	GGG GGA GGC ATG GCG GCG GGT GCG GGC GAG GAG AGT CTG TCG CGG CGA	7985
	Gly Gly Gly Met Ala Ala Gly Ala Gly Glu Glu Ser Leu Ser Arg Arg	
	2375 2380 2385 2390	
	GGG CTG CGG GCC ATG GAC CCC GAC GCG GCC GTC GAC GCG CTC CTG GGC	8033
	Gly Leu Arg Ala Met Asp Pro Asp Ala Ala Val Asp Ala Leu Leu Gly	
40	2395 2400 2405	
	GCC ATG GGC AGG AAC GAC GTG TCC GTC ACT GTC GTC GAC GTC GAC TGG	8081
	Ala Met Gly Arg Asn Asp Val Cys Val Thr Val Val Asp Val Asp Trp	
45	2410 2415 2420	
	GAG CGT TTC GCG CCC GCG ACG AAC GCC ATC CGT CCC GGG CGG CTG TTC	8129
	Glu Arg Phe Ala Pro Ala Thr Asn Ala Ile Arg Pro Gly Arg Leu Phe	
	2425 2430 2435	
50	GAC ACC GTG CCG GAG GCG CGG GAG GCC CTG ACG GCA GCC GGC ACC ACG	8177
	Asp Thr Val Pro Glu Ala Arg Glu Ala Leu Thr Ala Ala Gly Thr Thr	
	2440 2445 2450	
55	TCC GCG ACG CCG GAC GGC GCG CCC GAG CTG GCG CGG CGG TTG TCC ATC	8225
	Ser Ala Thr Pro Asp Gly Ala Pro Glu Leu Ala Arg Arg Leu Ser Met	
	2455 2460 2465 2470	

	CTG AAC GAG ACC GAA CGC CTG CCG AAG CTG GTC GAA CTC GTC CGT ACC	8273
	Leu Asn Glu Thr Glu Arg Leu Arg Lys Leu Val Glu Leu Val Arg Thr	
	2475 2480 2485	
5	GAG GCG GCC TTT GTG CTG CCG CAT CCG AAC ACG GAC GCC ATC GGC GCC	8321
	Glu Ala Ala Phe Val Leu Arg His Pro Asn Thr Asp Ala Ile Gly Ala	
	2490 2495 2500	
10	GAA CGC CCG TTC AAG TCG GCC GGT TTC GAC TCC CTG ACC TCC CTG GAA	8369
	Glu Arg Pro Phe Lys Ser Ala Gly Phe Asp Ser Leu Thr Ser Leu Glu	
	2505 2510 2515	
15	CTC CGC AAC CGC CTC AAT GCC GGC ACA GGC CTG AAG CTA CCC GCC ACC	8417
	Leu Arg Asn Arg Leu Asn Ala Gly Thr Gly Leu Lys Leu Pro Ala Thr	
	2520 2525 2530	
	GTC ATC TTC GAC CAC CCC AGC CCG ACC GCC CTG GCC AGA CTG CTG CTC	8465
	Val Ile Phe Asp His Pro Ser Pro Thr Ala Leu Ala Arg Leu Leu Leu	
	2535 2540 2545 2550	
20	GAC CGG CTG ACC GGC GCC GGA GCC CCC GCG CCC GCC GCC GAT GAG CCG	8513
	Asp Arg Leu Thr Gly Ala Gly Ala Pro Ala Pro Ala Ala Asp Glu Pro	
	2555 2560 2565	
25	CCA CTG CCC GTC GCC GTG GCC GAC GAC GAC CCG GTG GTC ATC GTC GGC	8561
	Pro Leu Pro Val Ala Val Ala Asp Asp Asp Pro Val Val Ile Val Gly	
	2570 2575 2580	
	ATG GCG TGC CGT TTC CCC GGT GGG GCG GGC ACC CCT GAG GCG CTG TGG	8609
	Met Ala Cys Arg Phe Pro Gly Gly Ala Gly Thr Pro Glu Ala Leu Trp	
	2585 2590 2595	
30	AAG CTG GTG ACC GAG GAG CGT GAC GTC ATA GGC GCC GCG CCC ACC GAC	8657
	Lys Leu Val Thr Glu Glu Arg Asp Val Ile Gly Ala Ala Pro Thr Asp	
	2600 2605 2610	
35	CGG GCG TGG GAC CTG GAT TCC GTC TAC GAC CCG GAG CCG GGT GTG GCG	8705
	Arg Gly Trp Asp Leu Asp Ser Val Tyr Asp Pro Glu Pro Gly Val Ala	
	2615 2620 2625 2630	
40	GGG AAG ACA TAT GTG CCG GAG GGG GGT TTT CTC CAC GAC GCG CCG GAG	8753
	Gly Lys Thr Tyr Val Arg Glu Gly Gly Phe Leu His Asp Ala Ala Glu	
	2635 2640 2645	
	TTC GAC GCG GAG TTC TTC GGG ATT TCG CCG CGT GAG CCG GTG GCG ATG	8801
	Phe Asp Ala Glu Phe Phe Gly Ile Ser Pro Arg Glu Ala Val Ala Met	
	2650 2655 2660	
45	GAT CCG CAG CAG CCG CTG TTG CTG GAG ACC TCC TGG GAG GCG ATC GAG	8849
	Asp Pro Gln Gln Arg Leu Leu Leu Glu Thr Ser Trp Glu Ala Ile Glu	
	2665 2670 2675	
50	CGG GCG GGT ATC GAC CCG CAC TCG CTG CAC GGC AGC CCG ACC GCG GTA	8897
	Arg Ala Gly Ile Asp Pro His Ser Leu His Gly Ser Arg Thr Gly Val	
	2680 2685 2690	
55	TAC GTC GGG CTG ACC CAT CAG GAG TAC GCC TCC CCG CTG CAC GAG GCC	8945
	Tyr Val Gly Leu Thr His Gln Glu Tyr Ala Ser Arg Leu His Glu Ala	
	2695 2700 2705 2710	

	CCG GAG GAG TAC GAA GGC TAT CTG CTC ACC GGC AAG TCG GCG AGC GTC	8993
	Pro Glu Glu Tyr Glu Gly Tyr Leu Leu Thr Gly Lys Ser Ala Ser Val	
	2715 2720 2725	
5	GTC TCC GGC CGC ATC TCG TAC ACG CTG GGG CTG GAG GGT CCT TCG CTC	9041
	Val Ser Gly Arg Ile Ser Tyr Thr Leu Gly Leu Glu Gly Pro Ser Leu	
	2730 2735 2740	
10	TCC ATC GAC ACC GCG TGT TCG TCG CTG GTC GCC CTG CAC AAC GCG	9089
	Ser Ile Asp Thr Ala Cys Ser Ser Leu Val Ala Leu His Asn Ala	
	2745 2750 2755	
	GCG CAG GCG TTG CCG GGT GGC GAG TGT GAC ATG GCG TTG GCC GGT GGT	9137
	Ala Gln Ala Leu Arg Gly Gly Glu Cys Asp Met Ala Leu Ala Gly Gly	
15	2760 2765 2770	
	GTG ACG GTG ATG GCG GCA CCC GGA TTG TTC GTG GAG TTT TCG CCG CAG	9185
	Val Thr Val Met Ala Ala Pro Gly Leu Phe Val Glu Phe Ser Arg Gln	
	2775 2780 2785 2790	
20	CGG GGG TTG GCG GCC GAT GGG CCG TGC AAG GCG TTC GCG GAT GGG GCG	9233
	Arg Gly Leu Ala Ala Asp Gly Arg Cys Lys Ala Phe Ala Asp Gly Ala	
	2795 2800 2805	
25	GAT GGG ACC GCT TGG GCC GAG GGT GCG GGG GTG GTG CTG GTG GAG CCG	9281
	Asp Gly Thr Ala Trp Ala Glu Gly Ala Gly Val Val Leu Val Glu Arg	
	2810 2815 2820	
	TTG TCG GAT GCC CCG CCG TTG GGG CAT CCG GTG TTG GCG GTG GTG TGT	9329
	Leu Ser Asp Ala Arg Arg Leu Gly His Pro Val Leu Ala Val Val Cys	
30	2825 2830 2835	
	GGG TCG GCG GTG AAT CAG GAC GGT GCG TCG AAT GGT TTG ACG GCG CCG	9377
	Gly Ser Ala Val Asn Gln Asp Gly Ala Ser Asn Gly Leu Thr Ala Pro	
	2840 2845 2850	
35	AGT GGT CCG TCG CAG GAG CCG GTG ATT CGT CAG CCG TTG GCG AAT GCG	9425
	Ser Gly Pro Ser Gln Glu Arg Val Ile Arg Gln Ala Leu Ala Asn Ala	
	2855 2860 2865 2870	
	CGG TTG ACG GTG GCG GAT GTG GAT GTG GTG GAG GCG CAT GCG ACG GCG	9473
	Arg Leu Thr Val Ala Asp Val Asp Val Val Glu Ala His Gly Thr Gly	
40	2875 2880 2885	
	ACG CCG CTG GGT GAT CCG ATC GAG GCG CAG GCG TTG CTG GCG ACG TAT	9521
	Thr Arg Leu Gly Asp Pro Ile Glu Ala Gln Ala Leu Leu Gly Thr Tyr	
45	2890 2895 2900	
	GGG CCG GAT CGT GAT GCT GAG TGT CCG GTG TGG TTG GGG TCG TTG AAG	9569
	Gly Arg Asp Arg Asp Ala Glu Cys Pro Val Trp Leu Gly Ser Leu Lys	
	2905 2910 2915	
50	TCG AAT ATT GGT CAT GCT CAG GCG GCT GCG GCG GTG GCT GGT GTG ATC	9617
	Ser Asn Ile Gly His Ala Gln Ala Ala Ala Gly Val Ala Gly Val Ile	
	2920 2925 2930	
55	AAG ATG GTG TTG GCG ATG CCG TAT GGG TGG TTG CCG CCG ACG TTG CAT	9665
	Lys Met Val Leu Ala Met Arg Tyr Gly Trp Leu Pro Arg Thr Leu His	
	2935 2940 2945 2950	

	GTG GAT GAG CCG AGC CCG CAT GTG GAC TGG TCG GCT GGT GGT GTG CCG Val Asp Glu Pro Ser Arg His Val Asp Trp Ser Ala Gly Gly Val Arg 2955 2960 2965	9713
5	TTG CTG ACC GAG GCG CCG GAG TGG CCG GGG GTG GAC CCG CCG CGT CCG Leu Leu Thr Glu Ala Arg Glu Trp Pro Gly Val Asp Arg Pro Arg Arg 2970 2975 2980	9761
10	GCG GCG GTC TCC GCC TTC GGT GTC AGT GGT ACC AAC GCC CAT CTG ATC Ala Ala Val Ser Ala Phe Gly Val Ser Gly Thr Asn Ala His Leu Ile 2985 2990 2995	9809
15	CTC GAA GCC CCC GAA GCC CTC GAA GCC CTC GAA GCC ACC GAC GCC CCC Leu Glu Ala Pro Glu Ala Leu Glu Ala Leu Glu Ala Thr Asp Ala Pro 3000 3005 3010	9857
	GAA GCC CCC GAA GCC CCC GAA GCC CCC GAC GTC ACC GAC GTC ACC GAA Glu Ala Pro Glu Ala Pro Glu Ala Pro Asp Val Thr Asp Val Thr Glu 3015 3020 3025 3030	9905
20	GCC CTC GAA GCC CCC GAC GCC ACC GAG GCG GAG GGT GCG AAG GCT CCT Ala Leu Glu Ala Pro Asp Ala Thr Glu Ala Glu Gly Ala Lys Ala Pro 3035 3040 3045	9953
25	GGC AGT CCC GAA GAG GCA CAG CCT GCT GTG GGT GTG GTG CCG GTG GTG Gly Ser Pro Glu Glu Ala Gln Pro Ala Val Gly Val Val Pro Val Val 3050 3055 3060	10001
30	GTT TCG GGG CGT TCG CCG GTG GTG GTG CCG GAG GCT GCG GGC CCG TTG Val Ser Gly Arg Ser Arg Val Val Val Arg Glu Ala Ala Gly Arg Leu 3065 3070 3075	10049
	GCG GAG GTG GTG GAG GCC GGT GGT GTG GCG CTG GCG GAT GTG CCG GTG Ala Glu Val Val Glu Ala Gly Gly Val Gly Leu Ala Asp Val Ala Val 3080 3085 3090	10097
35	ACG ATG GCG GGC CCG TCG CCG TTT GCG TAT CCG GCG GTT GTG CTG GCT Thr Met Ala Gly Arg Ser Arg Phe Gly Tyr Arg Ala Val Val Leu Ala 3095 3100 3105 3110	10145
40	CGG GGT GAG GCT GAG CTT GCC GCG CGT TTG CCG GCG TTG GCG GCG GGT Arg Gly Glu Ala Glu Leu Ala Gly Arg Leu Arg Ala Leu Ala Gly Gly 3115 3120 3125	10193
45	GAT CCG GAC GCG GGT GTG GTC ACC GGT GCG GTG GTG GAC CCG GAG ACG Asp Pro Asp Ala Gly Val Val Thr Gly Ala Val Val Asp Pro Glu Thr 3130 3135 3140	10241
	GGG TCC GGT GGT GCG GGC GTG GTG TTG GTT TTC CCT GGT CAG GCG ACG Gly Ser Gly Gly Gly Val Val Leu Val Phe Pro Gly Gln Gly Thr 3145 3150 3155	10289
50	CAG TGG GTG GGG ATG GGT GCG GCG CTG CTG GGG TCT TCG GAG GTG TTT Gln Trp Val Gly Met Gly Ala Gly Leu Leu Gly Ser Ser Glu Val Phe 3160 3165 3170	10337
55	GCG GCG TCG ATG CCG GAG TGT GCG CCG GCG CTG AGT GTT CAT GTG GAG Ala Ala Ser Met Arg Glu Cys Ala Arg Ala Leu Ser Val His Val Glu 3175 3180 3185 3190	10385

	TGG GAT TTG CTG GAG GTG GTG TCG GGC GGG GCC GGG TTG GAG CCG GTG	10433
	Trp Asp Leu Leu Glu Val Val Ser Gly Gly Ala Gly Leu Glu Arg Val	
	3195 3200 3205	
5	GAT GTG GTG CAG CCC GTG ACG TGG GCG GTG ATG GTG TCG CTG GCC CCG	10481
	Asp Val Val Gln Pro Val Thr Trp Ala Val Met Val Ser Leu Ala Arg	
	3210 3215 3220	
10	TAC TGG CAG GCG ATG GGT GTG GAC GTG GCT GCG GTG CTG GGT CAT TCC	10529
	Tyr Trp Gln Ala Met Gly Val Asp Val Ala Ala Val Val Gly His Ser	
	3225 3230 3235	
15	CAG GGG GAG ATC GCT GCT GCC ACG GTG GCG GGG GCG TTG TCG CTG GAG	10577
	Gln Gly Glu Ile Ala Ala Ala Thr Val Ala Gly Ala Leu Ser Leu Glu	
	3240 3245 3250	
	GAT GCG GCG GCT GTG GTC GCT CTG CCG GCG GGG TTG ATT GGC CCG TAT	10625
	Asp Ala Ala Ala Val Val Ala Leu Arg Ala Gly Leu Ile Gly Arg Tyr	
	3255 3260 3265 3270	
20	CTG GCG GGT CGT GGT GCG ATG GCG GCT GTT CCG CTG CCT GCC GCG GAG	10673
	Leu Ala Gly Arg Gly Ala Met Ala Ala Val Pro Leu Pro Ala Gly Glu	
	3275 3280 3285	
25	GTC GAG GCC GGG CTG GCG AAG TGG CCC GGA GTA CAG GTA GCC GCG GTC	10721
	Val Glu Ala Gly Leu Ala Lys Trp Pro Gly Val Gln Val Ala Ala Val	
	3290 3295 3300	
30	AAC GGT CCG GCG TCC ACG GTG GTT TCC GGG GAT CCG CCG GCG GTG GCC	10769
	Asn Gly Pro Ala Ser Thr Val Val Ser Gly Asp Arg Arg Ala Val Ala	
	3305 3310 3315	
	GGT TAT GTG GCC GTC TGT CAG GCG GAG GGT GTG CAG GCT CCG TTG ATA	10817
	Gly Tyr Val Ala Val Cys Gln Ala Glu Gly Val Gln Ala Arg Leu Ile	
	3320 3325 3330	
35	CCG GTG GAC TAC GCC TCT CAC TCC CCG CAT GTG GAG GAC CTG AAG GGC	10865
	Pro Val Asp Tyr Ala Ser His Ser Arg His Val Glu Asp Leu Lys Gly	
	3335 3340 3345 3350	
40	GAG TTG GAG CCG GTG CTG TCC GGT ATC CCG CCC CCG AGT CCG CCG GTG	10913
	Glu Leu Glu Arg Val Leu Ser Gly Ile Arg Pro Arg Ser Pro Arg Val	
	3355 3360 3365	
45	CCG GTG TGT TCC ACC GTC GCC GGA GAG CAG CCG GCG GAG CCG GTT TTC	10961
	Pro Val Cys Ser Thr Val Ala Gly Glu Gln Pro Gly Glu Pro Val Phe	
	3370 3375 3380	
50	GAT GCG GCG TAT TGG TTC CGT AAT CTG CCG AAC CCG GTT GAG TTC TCC	11009
	Asp Ala Gly Tyr Trp Phe Arg Asn Leu Arg Asn Arg Val Glu Phe Ser	
	3385 3390 3395	
55	GCG GTG GTC GGT GGT TTG TTG GAG CAG GGC CAC CGT CCG TTC ATC GAG	11057
	Ala Val Val Gly Gly Leu Leu Glu Gln Gly His Arg Arg Phe Ile Glu	
	3400 3405 3410	
	GTC AGT GCC CAC CCG GTA CTC GTC CAT GCC ATT GAG CAG ACG GCC GAG	11105
	Val Ser Ala His Pro Val Leu Val His Ala Ile Glu Gln Thr Ala Glu	
	3415 3420 3425 3430	

	GCC GCG GAC CGG AGT GTC CAT GCC ACC GGA ACC CTG CGC CGC CAG GAC	11153
	Ala Ala Asp Arg Ser Val His Ala Thr Gly Thr Leu Arg Arg Gln Asp	
	3435 3440 3445	
5	GAC AGC CCG CAC CGC CTG CTG ACC TCC ACC GCC GAG GCC TGG GCC CAC	11201
	Asp Ser Pro His Arg Leu Leu Thr Ser Thr Ala Glu Ala Trp Ala His	
	3450 3455 3460	
10	GGC GCC ACC CTC ACC TGG GAC CCC GCC CTG CCC CCA GGT CAC CTC ACC	11249
	Gly Ala Thr Leu Thr Trp Asp Pro Ala Leu Pro Pro Gly His Leu Thr	
	3465 3470 3475	
	ACC CTC CCC ACC TAC CCC TTC AAC CAC CAC CAC TAC TGG GCC GTG ACA	11297
	Thr Leu Pro Thr Tyr Pro Phe Asn His His His Tyr Trp Ala Val Thr	
15	3480 3485 3490	
	TCC CCC GCC GGA GTC GGC GAC GCG GCT GCG GGC CGG TTC GGT ATG ACC	11345
	Ser Pro Ala Gly Val Gly Asp Ala Ala Ala Gly Arg Phe Gly Met Thr	
	3495 3500 3505 3510	
20	TGG GAG GAC CAC CCC TTC CTC CGT GGC GGG TTA CCC CTG GCC GAC TCC	11393
	Trp Glu Asp His Pro Phe Leu Arg Gly Gly Leu Pro Leu Ala Asp Ser	
	3515 3520 3525	
25	GGT GAG CGG GTG TTC GCC GGG CGG CTG GCG GGC TCC GAG CAC GAC TGG	11441
	Gly Glu Arg Val Phe Ala Gly Arg Leu Ala Gly Ser Glu His Asp Trp	
	3530 3535 3540	
	CTG ACG GAC CAT GCC GTG TCC GGG GTG ACG TTG CTG CCG GGT ACG GCC	11489
	Leu Thr Asp His Ala Val Ser Gly Val Thr Leu Leu Pro Gly Thr Ala	
30	3545 3550 3555	
	TTC GTG GAG TTC GCG CTG CAC GCG GGA GCC GCC ACC GGC TGC GGG CGG	11537
	Phe Val Glu Phe Ala Leu His Ala Gly Ala Ala Thr Gly Cys Gly Arg	
	3560 3565 3570	
35	CTG GAA GAG CTG AGC GTT GAG GCG CCG TTG GTC TTG CCC GCC GCC GGT	11585
	Leu Glu Glu Leu Ser Val Glu Ala Pro Leu Val Leu Pro Ala Ala Gly	
	3575 3580 3585 3590	
40	GGT GTG CCG GTG CAG ATG AGG GTG TCG GCC GCC GAC GAG TCG GGA CGG	11633
	Gly Val Arg Val Gln Met Arg Val Ser Ala Ala Asp Glu Ser Gly Arg	
	3595 3600 3605	
	CGG AGG GTC GCC ATC CAC TCG GCC CCG GAA GCC GCC GTC CAC TCG GCC	11681
	Arg Arg Val Ala Ile His Ser Ala Pro Glu Ala Ala Val His Ser Ala	
45	3610 3615 3620	
	GCA GAA GGC GGC GAC TCG GCC GGT GTC TGG ACG CGG CAC GGC GAG GGC	11729
	Ala Glu Gly Gly Asp Ser Ala Gly Val Trp Thr Arg His Gly Glu Gly	
	3625 3630 3635	
50	ACG CTC GTG CCG GAC CCG GAG CCC ACG CCT CCG GAC GCC GAC TGG GCG	11777
	Thr Leu Val Pro Asp Pro Glu Pro Thr Pro Pro Asp Ala Asp Trp Ala	
	3640 3645 3650	
55	CGG GCC TGG CCG CCC GCC GGG GAA CGC GTC GAA CCG GCC GAG CTC TAC	11825
	Arg Ala Trp Pro Pro Ala Gly Glu Arg Val Glu Pro Ala Glu Leu Tyr	
	3655 3660 3665 3670	

	GAA CGG TTC GGG GCC CTG GGC TAC GAG TAC GGT GAG GCG TTC GCG GGC	11873
	Glu Arg Phe Gly Ala Leu Gly Tyr Glu Tyr Gly Glu Ala Phe Ala Gly	
	3675 3680 3685	
5	GTG CGC GCC GTA TGG CGG CAG CCG GAC GCG CTG CTC GCC GAG GTG CTC	11921
	Val Arg Ala Val Trp Arg Gln Pro Asp Ala Leu Leu Ala Glu Val Leu	
	3690 3695 3700	
10	CTG CCC GAC CGG GCC TCG ACC GGT GCC GCG CGG TTC GGT GTG CAC CCC	11969
	Leu Pro Asp Arg Ala Ser Thr Gly Ala Gly Arg Phe Gly Val His Pro	
	3705 3710 3715	
	GCG CTG CTG GAC GCG GCG CTG CAG CCG TGG ATC GCC GGT GGT CTC CTC	12017
	Ala Leu Leu Asp Ala Ala Leu Gln Pro Trp Ile Ala Gly Gly Leu Leu	
15	3720 3725 3730	
	GAA GTG CCG GAG GAC GCA GTG CTG CTG CCC TTC GCC TGG CAG GGA GTG	12065
	Glu Val Pro Glu Asp Ala Val Leu Leu Pro Phe Ala Trp Gln Gly Val	
	3735 3740 3745 3750	
20	TCG CTC TAC GCG ACG GGT GCC GGT GCT CTG CGG GTG CCG CTG ACG AAG	12113
	Ser Leu Tyr Ala Thr Gly Ala Gly Ala Leu Arg Val Arg Leu Thr Lys	
	3755 3760 3765	
25	GCG GGT GAC GGG GCG GTC TCG CTC CAG GCC GCA GAC ACG TCC GCG GCG	12161
	Ala Gly Asp Gly Ala Val Ser Leu Gln Ala Ala Asp Thr Ser Gly Ala	
	3770 3775 3780	
	GCC GTG CTC TCC TTG GGG GCC CTG GTG ATG CGT CCG CTG GCG CCG CCG	12209
	Ala Val Leu Ser Leu Gly Ala Leu Val Met Arg Pro Leu Ala Arg Arg	
30	3785 3790 3795	
	AAG CTG GAC GTG CTG CTC GCG ACG GAC GCC GCG GAA CCG TCG CTG TAC	12257
	Lys Leu Asp Val Leu Leu Gly Thr Asp Ala Gly Glu Arg Ser Leu Tyr	
	3800 3805 3810	
35	CGC GTC GAG TGG CAG CCG CGG CTC CTG CCC GCC GCG CCG CCG CCG TCC	12305
	Arg Val Glu Trp Gln Pro Arg Leu Leu Pro Ala Gly Pro Pro Arg Ser	
	3815 3820 3825 3830	
40	TGG GCG GTG CTC GCG CCC GAC GCG GAC CCG CTC GCC GCG ACG CCG GCG	12353
	Trp Ala Val Leu Gly Pro Asp Ala Asp Arg Leu Ala Gly Thr Pro Gly	
	3835 3840 3845	
	CTG GCG GAT CAG CCG GAC GGT GGG CCC ACC GCG CTG TAC CCG GAG GTG	12401
	Leu Gly Asp Gln Pro Asp Gly Gly Pro Thr Ala Leu Tyr Pro Glu Val	
45	3850 3855 3860	
	CGG GCG CTG CCG AAG GCG CTG GCG GCG GCG CCG CCG CCG GAA GCG	12449
	Arg Ala Leu Arg Lys Ala Leu Ala Ala Gly Ala Pro Arg Pro Glu Ala	
	3865 3870 3875	
50	GTC GTA CTG CCG GTG CTC TCC GGG GCC GCG GCC ACT CCG GAG TCG GTC	12497
	Val Val Leu Pro Val Leu Ser Gly Ala Gly Ala Thr Pro Glu Ser Val	
	3880 3885 3890	
55	CGG CAG ACA ACG GAG CCG TGT CTG ACC GCG CTC CAG GAC TGG CTG GAC	12545
	Arg Gln Thr Thr Glu Arg Cys Leu Thr Ala Leu Gln Asp Trp Leu Asp	
	3895 3900 3905 3910	

	GCC GAG GAG TTG GTG GAC ACA CCG CTC ATA GTG CTC ACC AGG GGA GCC Ala Glu Glu Leu Val Asp Thr Pro Leu Ile Val Leu Thr Arg Gly Ala 3915 3920 3925	12593
5	GTC GCC GCC GTA CCG GGG GAG GAG ATC GGG GAC CTG GCG TGT GCG GGG Val Ala Ala Val Pro Gly Glu Glu Ile Gly Asp Leu Ala Cys Ala Gly 3930 3935 3940	12641
10	GTG TGG GGC CTG GTG AGG TCC GCG CCG TCC GAG CAC CCG GGC CCG TTC Val Trp Gly Leu Val Arg Ser Ala Arg Ser Glu His Pro Gly Arg Phe 3945 3950 3955	12689
15	GCC CTC GTC GAC ACC GAC GGG CAT CCG GAC GAC CCG ACC GCG CTG CCC Ala Leu Val Asp Thr Asp Gly His Pro Asp Asp Arg Thr Ala Leu Pro 3960 3965 3970	12737
20	CTC GCG CTG CCG GCG GTC CTC GAC GGC GCC GGC CAG CTC TCC CTG CCG Leu Ala Leu Arg Ala Val Leu Asp Gly Ala Gly Gln Leu Ser Leu Arg 3975 3980 3985 3990	12785
25	GCC GGC ACC GCC CCG ACC CCG GTC CTC CTC CCG GCC GGG ACC CCG GAG Ala Gly Thr Ala Arg Thr Pro Val Leu Leu Arg Ala Gly Thr Pro Glu 3995 4000 4005	12833
30	GAG CAG CCG GGT CCG GCA TTC GAC CCG GCG GGC ACG GTC CTG GTG ACG Glu Gln Arg Gly Pro Ala Phe Asp Pro Ala Gly Thr Val Leu Val Thr 4010 4015 4020	12881
35	GGC GCG ACC GGC ACG CTC GGG CCG CTG CTG GCC CCG CAT CTG GCC GCC Gly Ala Thr Gly Thr Leu Gly Arg Leu Leu Ala Arg His Leu Ala Ala 4025 4030 4035	12929
40	GAG CAC GGT GTG CCG CAT CTG CTG CTG CTG AGC CCG GGC GGC CCG GCT Glu His Gly Val Arg His Leu Leu Leu Leu Ser Arg Gly Gly Arg Ala 4040 4045 4050	12977
45	GCC GAA GGC GCG GAC GAA CTC GCC GCG GAA CTG GCC GGG TTG GAA GCC Ala Glu Gly Ala Asp Glu Leu Ala Ala Glu Leu Ala Gly Leu Glu Ala 4055 4060 4065 4070	13025
50	GAG CCG TGC TTC GCG GCC TGT GAC GCG GCG GAC CCG GAG GCC CTG GCA Glu Pro Cys Phe Ala Ala Cys Asp Ala Ala Asp Arg Glu Ala Leu Ala 4075 4080 4085	13073
55	CGG GTG CTG GCG GAG GTG CCG GCC GAC CCG CCG CTG ACC GGA GTG ATC Arg Val Leu Ala Glu Val Pro Ala Asp Arg Pro Leu Thr Gly Val Ile 4090 4095 4100	13121
60	CAC CCG GCC GGG GTG CTC GAC GAC GGC ACA CTC GAC GCG CTG ACC CCG His Ala Ala Gly Val Leu Asp Asp Gly Thr Leu Asp Ala Leu Thr Pro 4105 4110 4115	13169
65	GAA CCG ATC GGT ACC GTC ATG CCG CCG AAG GCG GAC GCG GCG CTG AAC Glu Arg Ile Gly Thr Val Met Arg Pro Lys Ala Asp Ala Ala Leu Asn 4120 4125 4130	13217
70	CTG CAC GAA CTG ACC CCG ACC AGC CCG CTG TCG GTG TTC GCG GTC TTC Leu His Glu Leu Thr Arg Thr Ser Pro Leu Ser Val Phe Ala Val Phe 4135 4140 4145 4150	13265

	TCG GGC GCT GCC GGC ATC CTG GGC CGC CCC GGA CAG GCC AAC TAC GCC	13313
	Ser Gly Ala Ala Gly Ile Leu Gly Arg Pro Gly Gln Ala Asn Tyr Ala	
	4155 4160 4165	
5	GCC GCC AAC ACC TTC CTC GAC GCG CTC GCG CAG CAC CGC CGC GCC CAC	13361
	Ala Ala Asn Thr Phe Leu Asp Ala Leu Ala Gln His Arg Arg Ala His	
	4170 4175 4180	
10	GGC CTC CCC GCC CTG TCG CTC GCC TGG GGG CTG TGG GGC GGG GCG ACC	13409
	Gly Leu Pro Ala Val Ser Leu Ala Trp Gly Leu Trp Gly Gly Ala Thr	
	4185 4190 4195	
	GGC ATG ACC GGC CAT CTG TCC GGC ACC GAT CTG CGC CGG ATG CGC AGG	13457
	Gly Met Thr Gly His Leu Ser Gly Thr Asp Leu Arg Arg Met Arg Arg	
15	4200 4205 4210	
	TCC GGT ATC GCG CCG ATG ACC CAC GAC CAG GGG CTC GCC CTG TTC GAC	13505
	Ser Gly Ile Ala Pro Met Thr His Asp Gln Gly Leu Ala Leu Phe Asp	
	4215 4220 4225 4230	
20	CGA GCG CTC GCC GCC TCG GCC GAG GAC CCG CTG CTC GTA CCG ATG CGG	13553
	Arg Ala Leu Ala Ala Ser Ala Glu Asp Pro Leu Leu Val Pro Met Arg	
	4235 4240 4245	
25	CTG GAC CTG GCC GCC CTC GTC CCG GAG CCG GCC GAG CAC GGG CCG GAC	13601
	Leu Asp Leu Ala Ala Leu Val Arg Glu Arg Ala Glu His Gly Pro Asp	
	4250 4255 4260	
	GCG GTG CCC GGA CCG CTG CTC GGG CTG CTG CCC GCC CGG GCC GCG GTG	13649
	Ala Val Pro Gly Pro Leu Leu Gly Leu Leu Pro Ala Arg Ala Ala Val	
30	4265 4270 4275	
	CGG CAG GCG GCG GCA CCG GTA CCG GGC GGA GCC CCC GCC CCC GCC GGC	13697
	Arg Gln Ala Ala Ala Pro Val Arg Gly Gly Ala Pro Ala Pro Ala Gly	
	4280 4285 4290	
35	GGC GAG GGG ACG GCC GAG CCG CTG GCC GGG CTC GGG GAG GAG GCC AGG	13745
	Gly Glu Gly Thr Ala Glu Arg Leu Ala Gly Leu Gly Glu Glu Ala Arg	
	4295 4300 4305 4310	
	CTG CGC GAG CTG GTG AGG CTG GTC CCG GCC GAG GTG TCG GGC GTG CTG	13793
	Leu Arg Glu Leu Val Arg Leu Val Arg Ala Glu Val Ser Gly Val Leu	
40	4315 4320 4325	
	GGC TAC TCG GGC CCG GAC GCG GTG GAG CCC GGG CGC CCG TTC AAG GAT	13841
	Gly Tyr Ser Gly Pro Asp Ala Val Glu Pro Gly Arg Pro Phe Lys Asp	
45	4330 4335 4340	
	CTC GCC TTC GAC TCG CTG ACC GCC GTG GAG CTG CGC AAC CGC CTC GGC	13889
	Leu Gly Phe Asp Ser Leu Thr Ala Val Glu Leu Arg Asn Arg Leu Gly	
	4345 4350 4355	
50	GCC GCC ACC GGG CTG CCG CTG CCG ACC GCG CTG GTC TTC GAC CGC CCG	13937
	Ala Ala Thr Gly Leu Arg Leu Pro Thr Ala Leu Val Phe Asp Arg Pro	
	4360 4365 4370	
55	ACG TCC CAG GCA GTG GCC GAG TAC CTC GCT GCC GAA CTG GCC GGA CCG	13985
	Thr Ser Gln Ala Val Ala Glu Tyr Leu Ala Ala Glu Leu Ala Gly Pro	
	4375 4380 4385 4390	

	CGG GAC GGC GGC GAC ACC GCG GCC GCC GCG TTC GAG GGC CTG GAG GCG Arg Asp Gly Gly Asp Thr Ala Ala Ala Ala Phe Glu Gly Leu Glu Ala 4395 4400 4405	14033
5	CTG GCC GCG GCG GTG GGC GCG CTG GCC GAG GAC GAT CTG CGG CGC GAC Leu Ala Ala Ala Val Gly Ala Leu Ala Glu Asp Asp Leu Arg Arg Asp 4410 4415 4420	14081
10	GTG CTC CGG CGG CGA CTG ACC GAA CTG GCC GCC GCG CTC ACC CCG CAG Val Leu Arg Arg Arg Leu Thr Glu Leu Ala Ala Ala Leu Thr Pro Gln 4425 4430 4435	14129
15	GGC CGG AAC CCC TCC GCG CCC GCA CCC GCC CCG TCC GAT CTG GAC GAG Gly Arg Asn Pro Ser Ala Pro Ala Pro Ala Pro Ser Asp Leu Asp Glu 4440 4445 4450	14177
	CGG CTG GAC TCC GCG AAC GAC GAC GAC CTC TTC GCC TTC ATC GAG GAG Arg Leu Asp Ser Ala Asn Asp Asp Asp Leu Phe Ala Phe Ile Glu Glu 4455 4460 4465 4470	14225
20	CAG CTT TGA GCAGCGAGAA CGACAGCAGC GAGAACGACG GCGACGACAC Gln Leu *	14274
	GGCCGGGGCA GCTCCGGGGA CGGCTCCGGG GGCCTCCCC CGGCAGGACG ACCGGGTCAG	14334
25	GGAGTATCTG AAGCGG GTG ACC GCC GAA CTG GTC GCC ACC CGC AAG CGG Met Thr Ala Glu Leu Val Ala Thr Arg Lys Arg 1 5 10	14383
30	CTC GGC GCG CTG GAG GAG GCG GCC GCG GAA CCG ATC GCC GTC GTC GCG Leu Gly Ala Leu Glu Glu Arg Ala Arg Glu Pro Ile Ala Val Val Ala 15 20 25	14431
	ATG AGC TGC CGC TAC CCG GGC GGG GTG ACG ACC CCC GAG GAC CTG TGG Met Ser Cys Arg Tyr Pro Gly Gly Val Thr Thr Pro Glu Asp Leu Trp 30 35 40	14479
35	CGG CTT CTC GCG GAC GAA CGC GAC GCC GTA TCC GGA CTT CCC CGG GAC Arg Leu Leu Ala Asp Glu Arg Asp Ala Val Ser Gly Leu Pro Arg Asp 45 50 55	14527
40	CGC GGC TGG GAC CTG GAC GCC CTC TAC GAC CCC GAC GGC GGC CCC GGC Arg Gly Trp Asp Leu Asp Ala Leu Tyr Asp Pro Asp Gly Gly Pro Gly 60 65 70 75	14575
45	ACC AGC TAC GCC CGC GAA GGC GGC TTC CTG AGC CAC TGC GCC GGA TTC Thr Ser Tyr Ala Arg Glu Gly Gly Phe Leu Ser His Cys Ala Gly Phe 80 85 90	14623
	GAC GCG GAG TTC TTC GGC ATC TCC CCG GCG GAG GCG CTG GCG ATG GAC Asp Ala Glu Phe Phe Gly Ile Ser Pro Arg Glu Ala Leu Ala Met Asp 95 100 105	14671
50	CCG CAG CAG CGG CTG CTG CTG GAG ACC TCC TGG GAG GCC CTG GAA CGC Pro Gln Gln Arg Leu Leu Leu Glu Thr Ser Trp Glu Ala Leu Glu Arg 110 115 120	14719
55	GCC GGA GTC ACC GCC GAC CGC GCC CCG GGC AGC CGG ACG GGC GTG TAC Ala Gly Val Thr Ala Asp Arg Ala Arg Gly Ser Arg Thr Gly Val Tyr	14767

	125	130	135	
5	GCG GGC GTC ATG TAC GAC GAC TAC GGC GCC CGG GTG CTG TAC GGC GCC Ala Gly Val Met Tyr Asp Asp Tyr Gly Ala Arg Val Leu Tyr Gly Ala 140 145 150 155	14815		
	GCC GCC GGC CCG CCC GAG GAC CTG GAG GGT TAT CTC GTC AAC GGC AGC Gly Ala Gly Pro Pro Glu Asp Leu Glu Gly Tyr Leu Val Asn Gly Ser 160 165 170	14863		
10	GCG GGC AGC ATC GCC TCC GGC CGT GTC TCC TAC ACG TTC GGG CTG CGC Ala Gly Ser Ile Ala Ser Gly Arg Val Ser Tyr Thr Phe Gly Leu Arg 175 180 185	14911		
15	GGC CCC GCG GTC ACC GTC AAT ACG GCC TGT TCG TCG TCA CTG GTG TCG Gly Pro Ala Val Thr Val Asn Thr Ala Cys Ser Ser Ser Leu Val Ser 190 195 200	14959		
20	CTC CAT CTG GCG GTG CGT GCC CTG CGG AAC GGC GAG TGC GAC ATG GCA Leu His Leu Ala Val Arg Ala Leu Arg Asn Gly Glu Cys Asp Met Ala 205 210 215	15007		
	CTG GCC GGC GGG GCG ACG GTG CTG TCC ACC CCC ACC GTG CTC GTG GAC Leu Ala Gly Gly Ala Thr Val Leu Ser Thr Pro Thr Val Leu Val Asp 220 225 230 235	15055		
25	TTC TCC CGC CAG CGC GGT CTG GCC CCC GAC GGC CGC TGC AAG GCG TTC Phe Ser Arg Gln Arg Gly Leu Ala Pro Asp Gly Arg Cys Lys Ala Phe 240 245 250	15103		
30	GCC GAC TCC GCC GAC GGC ACC TCC TGG GCC GAG GGC GCC GGA ATG CTG Ala Asp Ser Ala Asp Gly Thr Ser Trp Ala Glu Gly Ala Gly Met Leu 255 260 265	15151		
35	CTG CTC CAG CGG CTG TCC GAC GCC CGC CGC GAG GGG CGC CCC GTG CTG Leu Leu Gln Arg Leu Ser Asp Ala Arg Arg Glu Gly Arg Pro Val Leu 270 275 280	15199		
	GCC GTC ATT CGC GGC TCG GCC GTC AAC CAG GAC GGC GCC AGC AAC GGA Ala Val Ile Arg Gly Ser Ala Val Asn Gln Asp Gly Ala Ser Asn Gly 285 290 295	15247		
40	CTG ACC GCC CCC AAC GGG CGG GCG CAG CGG CAG GTC ATC GAG GAC GCG Leu Thr Ala Pro Asn Gly Arg Ala Gln Arg Gln Val Ile Glu Asp Ala 300 305 310 315	15295		
45	CTG CGC GAC GCC GGG GTC GGC CCC GAC CAG GTG GAC GCG GTC GAG GCG Leu Arg Asp Ala Gly Val Gly Pro Asp Gln Val Asp Ala Val Glu Ala 320 325 330	15343		
50	CAT GGC ACC GGT ACC GAG CTG GGC GAC CCC ATC GAG GCC GGG GCG CTG His Gly Thr Gly Thr Glu Leu Gly Asp Pro Ile Glu Ala Gly Ala Leu 335 340 345	15391		
	CTC GCC ACC TAT GGA ACG GCC CGT ACG GCG GAG CGC CCG CTG TGG CTC Leu Ala Thr Tyr Gly Thr Ala Arg Thr Ala Glu Arg Pro Leu Trp Leu 350 355 360	15439		
55	GGC TCC CTG AAG TCC AAC ATC GGG CAC ACC CAG GCC GCC GCC GGT GTT Gly Ser Leu Lys Ser Asn Ile Gly His Thr Gln Ala Ala Ala Gly Val	15487		

	365	370	375	
5	GCG GGC GTC ATC AAG ATG GTG CTG GCG ATG CCG CAC GGC CGG CTG CCC Ala Gly Val Ile Lys Met Val Leu Ala Met Arg His Gly Arg Leu Pro 380 385 390 395			15535
10	CGC ACC CTG CAC GTG GAC CCG CCC ACC ACC CCG GTG GAC TGG GAG AAG Arg Thr Leu His Val Asp Arg Pro Thr Thr Arg Val Asp Trp Glu Lys 400 405 410			15583
15	GGC GGG GTG CCG CTC CTC ACG GAG CCG GTG CCA TGG CCG GGG GAA GCG Gly Gly Val Arg Leu Leu Thr Glu Pro Val Pro Trp Pro Gly Glu Ala 415 420 425			15631
20	GGG GAG CCG CGT CGC GCG GGC GTG TCC TCC TTC GGC GCG AGC GGC ACG Gly Glu Pro Arg Arg Ala Gly Val Ser Ser Phe Gly Ala Ser Gly Thr 430 435 440			15679
25	AAC GCG CAT GTG GTG CTG GAG AGC GTC CCG GCC GGT GAA CCG CCC GCC Asn Ala His Val Val Leu Glu Ser Val Pro Ala Gly Glu Pro Pro Ala 445 450 455			15727
30	GCC GGG CCG CCG GAG GAC ACA GGC GGC GCC TGG ACG GTC AGC GGC CGC Ala Gly Arg Pro Glu Asp Thr Gly Gly Ala Trp Thr Val Ser Gly Arg 460 465 470 475			15775
35	GGC CCG GCG GCC CTG CGC GCC CAG GCC GCC CCG CTG TAC GAC GCG CTC Gly Pro Ala Ala Leu Arg Ala Gln Ala Ala Arg Leu Tyr Asp Ala Leu 480 485 490			15823
40	ACC GGC ACC GGC ACC GGC ACC GGA CAG GGC GCC GGA CAG GGC GCC GGA Thr Gly Thr Gly Thr Gly Thr Gly Gln Gly Ala Gly Gln Gly Ala Gly 495 500 505			15871
45	CCC GGC ACC GCC GAG GTG GCC GGC GCG CTG GCC CAC GCC CGT ACC GCG Pro Gly Thr Ala Glu Val Ala Gly Ala Leu Ala His Ala Arg Thr Ala 510 515 520			15919
50	TTC CCG CAC CCG GCC GTC GTG CTC GGC GGA AAC CCG GCC GAA CTG CTC Phe Arg His Arg Ala Val Val Leu Gly Gly Asn Arg Ala Glu Leu Leu 525 530 535			15967
55	GCG GGG CTG CGC GAG CTG GCG GAG GAG GAG CAT CCC GGA CCC CCG GTG Ala Gly Leu Arg Glu Leu Ala Glu Glu Glu His Pro Gly Pro Arg Val 540 545 550 555			16015
60	GTC ACA GGG ACC GCC CCG GCC ACC GAG CCG CCG ACG GCC TTC CTC TTC Val Thr Gly Thr Ala Pro Ala Thr Glu Arg Arg Thr Ala Phe Leu Phe 560 565 570			16063
65	TCC GGG CAG GGC AGC CAG CCG GCC GGC TCC GGC CCG GGC CTG TAC CCG Ser Gly Gln Gly Ser Gln Arg Ala Gly Ser Gly Arg Gly Leu Tyr Arg 575 580 585			16111
70	CGC CAC CCG GTC TTC GCC CGC GCC CTC GAC GAG GTG TGC GCC GCG CTC Arg His Pro Val Phe Ala Arg Ala Leu Asp Glu Val Cys Ala Ala Leu 590 595 600			16159
75	GAA CCG CAT CTT CAC CGC CCC CTG CGT GAC CTG ATG TTC GCC GAG CCC Glu Pro His Leu His Arg Pro Leu Arg Asp Leu Met Phe Ala Glu Pro			16207

	605	610	615	
5	GGC AGC CCG GAA GCG GAG CCG CTC GAC CGC ACC GAG TTC ACC CAG CCC Gly Ser Pro Glu Ala Glu Pro Leu Asp Arg Thr Glu Phe Thr Gln Pro 620 625 630 635			16255
10	CGC CTG TTC GCG CTC CAG ACC GCC CTG TTC CGG CTG GCC GAG CAC CAC Ala Leu Phe Ala Leu Gln Thr Ala Leu Phe Arg Leu Ala Glu His His 640 645 650			16303
15	GGG CTG CGC GCC GAG GCG CTG TGC GGG CAC AGC GTC GGC GAG ATC GCG Gly Leu Arg Ala Glu Ala Leu Cys Gly His Ser Val Gly Glu Ile Ala 655 660 665			16351
20	GCC GCC CAT GCC GCC GGT GTG CTG ACC CTG CCC GAC GCG GCC CGT CTG Ala Ala His Ala Ala Gly Val Leu Thr Leu Pro Asp Ala Ala Arg Leu 670 675 680			16399
25	GTG GCC GCC CGG GGA CGG CTG ATG CAG GCC CTG CCG GCC GGC GGT GCC Val Ala Ala Arg Gly Arg Leu Met Gln Ala Leu Pro Ala Gly Gly Ala 685 690 695			16447
30	ATG GCC GCG CTG CGC GCC ACC GCC GAG GAG ATC GCA CCA CTG CTG GAG Met Ala Ala Leu Arg Ala Thr Ala Glu Glu Ile Ala Pro Leu Leu Glu 700 705 710 715			16495
35	CGC CGC GCG GGC GAA CTG GCG CTC GCC GCC GTC AAC GGC CCC TCC TCG Arg Arg Ala Gly Glu Leu Ala Leu Ala Val Asn Gly Pro Ser Ser 720 725 730			16543
40	GTG GTG GTG TCG GGC GAC GAG GCC GCC GTC CTG GAG CTA CTG GAG CAG Val Val Val Ser Gly Asp Glu Ala Ala Val Leu Glu Leu Leu Glu Gln 735 740 745			16591
45	TGG CGG GCC GAG GGC CGC GAG GCC AGG CGG CTC GCC GTC AGC CAT GCC Trp Arg Ala Glu Gly Arg Glu Ala Arg Arg Leu Ala Val Ser His Ala 750 755 760			16639
50	TTC CAT TCA CCG CGG ATG GAC GGA ATG TTG ACA CAG TTC GAC CGG GTC Phe His Ser Pro Arg Met Asp Gly Met Leu Thr Gln Phe Asp Arg Val 765 770 775			16687
55	GCT CGC ACC CTG ACG TTC GCT CCG CCG ACC ATT CCC CTC GTG TCC ACC Ala Arg Thr Leu Thr Phe Ala Pro Pro Thr Ile Pro Leu Val Ser Thr 780 785 790 795			16735
60	CTC ACC GGT ACG CCC GTC ACC GAG GAA ACC CTG TGC ACC GCG GAC CAC Leu Thr Gly Thr Pro Val Thr Glu Glu Thr Leu Cys Thr Ala Asp His 800 805 810			16783
65	TGG GTC CGC CAG GCG CGC GAG CCG GTG CGC TTC CTG GAC GCC ATG CGG Trp Val Arg Gln Ala Arg Glu Pro Val Arg Phe Leu Asp Ala Met Arg 815 820 825			16831
70	ACC CTG CGC GCC GAC GGG ATC GAC ACC TTC GTG GAA CTC GGC CCC GAC Thr Leu Arg Ala Asp Gly Ile Asp Thr Phe Val Glu Leu Gly Pro Asp 830 835 840			16879
75	GGC GTG CTG TCC GCC ATG GCC CGC GAC TGC GCG GAC GAC CGG CCC GAT Gly Val Leu Ser Ala Met Ala Arg Asp Cys Ala Asp Asp Arg Pro Asp			16927

EP 0 791 655 A2

	845	850	855	
5	GGC GAC ACA ACC GGG GCC GGG GAC GGG GAG ACC CCC GAT CCG CTG CTC Gly Asp Thr Thr Gly Ala Gly Asp Gly Glu Thr Pro Asp Pro Leu Leu 860 865 870 875			16975
10	ACC CTC CCG CTG CTG CGC CGC TCC GTG CCC GAG ACC GGC GAC GCC GAA Thr Leu Pro Leu Leu Arg Arg Ser Val Pro Glu Thr Gly Asp Ala Glu 880 885 890			17023
15	CAC CCC GGC GGC TTC GAA CGG GCC CTG GCC ACC GCC TAC GCA CAC GGC His Pro Gly Gly Phe Glu Arg Ala Leu Ala Thr Ala Tyr Ala His Gly 895 900 905			17071
20	GTC CCC CTG CGG CTC GCG CCC GCC CCC GAC GCC GCG TCC CTC GCC GTG Val Pro Leu Arg Leu Ala Pro Ala Pro Asp Ala Ala Ser Leu Ala Val 910 915 920			17119
25	GCC GCC GAA CTG CCC ACC TAC GCC TTC CAG CGC ACC CAC TAC TGG CTC Ala Ala Glu Leu Pro Thr Tyr Ala Phe Gln Arg Thr His Tyr Trp Leu 925 930 935			17167
30	GAC GCG CCC GCC GCC CCC GCC GCC CTC CCC GCC GGG CTC GAC GAC GCC Asp Ala Pro Ala Ala Pro Ala Ala Leu Pro Ala Gly Leu Asp Asp Ala 940 945 950 955			17215
35	GGT CAC CCG CTG CTC TCC GCG GCC CTC GAC CTG CCC GGC GGA CGC GGA Gly His Pro Leu Leu Ser Ala Ala Leu Asp Leu Pro Gly Gly Arg Gly 960 965 970			17263
40	ACG GTG TGG ACC GGA GCG CTC TCC GCG GCC ACC CTG CCC TGG GCC GCG Thr Val Trp Thr Gly Ala Leu Ser Ala Ala Thr Leu Pro Trp Ala Ala 975 980 985			17311
45	GAC CAC AGC GTG CAC GGC CGC ACC GTC CTG CCG GGC ACC GCC CTG CTC Asp His Ser Val His Gly Arg Thr Val Leu Pro Gly Thr Ala Leu Leu 990 995 1000			17359
50	GAC CTG GCG CTC CAC GCC GCC CCG CGC GTC GGC GAG TTG ACC TTC GAG Asp Leu Ala Leu His Ala Ala Pro Arg Val Gly Glu Leu Thr Phe Glu 1005 1010 1015			17407
55	GCG CCG CTG GTG CTG CCG GAG GAC GGA GAG GTC CCG CTG CGC GTC GTA Ala Pro Leu Val Leu Pro Glu Asp Gly Glu Val Arg Leu Arg Val Val 1020 1025 1030 1035			17455
60	CTC GCT GAA CCG GAC GCG AGC GGA GTA CGC GAA CTG TCT GTC CAC TCC Leu Ala Glu Pro Asp Ala Ser Gly Val Arg Glu Leu Ser Val His Ser 1040 1045 1050			17503
65	GCC GGC GAG GAC GGC GGC TGG ACC CCG CAC GCG ACA GCG GTC CTG GAC Ala Gly Glu Asp Gly Gly Trp Thr Arg His Ala Thr Ala Val Leu Asp 1055 1060 1065			17551
70	ACC GGC ACC ACC ACC GCC GGG GAG CCC GCC GGC GCA CCG CCC GCC GCA Thr Gly Thr Thr Ala Gly Glu Pro Ala Gly Ala Pro Pro Ala Ala 1070 1075 1080			17599
75	TGG CCG CCC GGG GAC GCC GAA CCC CTC GAC CTT GCC GCC GAG TAC GAG Trp Pro Pro Gly Asp Ala Glu Pro Leu Asp Leu Ala Ala Glu Tyr Glu			17647

EP 0 791 655 A2

	1085	1090	1095	
5	CGC TTC GCC GAC GCC GGC ATC GGA TAC GGC CCC GCC TTC CGC GGA CTG Arg Phe Ala Asp Ala Gly Ile Gly Tyr Gly Pro Ala Phe Arg Gly Leu 1100 1105 1110 1115			17695
10	CGC TCC GCC TGG CGC GAC GGC GAC GCG ATA CTG GCC GAC GTA CCG CTG Arg Ser Ala Trp Arg Asp Gly Asp Ala Ile Leu Ala Asp Val Arg Leu 1120 1125 1130			17743
15	CCC GGC GAA CTG GCC GGC GAA GCC GAC CGG TAC GGC ATC CAC CCG GCC Pro Gly Glu Leu Ala Gly Glu Ala Asp Arg Tyr Gly Ile His Pro Ala 1135 1140 1145			17791
20	CTG CTC GAC GCC GCC CTG CAC ACC GCG GCC GCC GCC CTG GGA GGG GCG Leu Leu Asp Ala Ala Leu His Thr Ala Ala Ala Leu Gly Gly Ala 1150 1155 1160			17839
25	CAC GGG ATG CTG CCG TTC ACG TGG AAC GGC GTC ACC CTC CAC GCC CGC His Gly Met Leu Pro Phe Thr Trp Asn Gly Val Thr Leu His Ala Arg 1165 1170 1175			17887
30	GGA GCG CAC GCC ATC CCG GTG CCG CTG ACC CCG GCC GGC CCC GAC GCG Gly Ala His Ala Ile Arg Val Arg Leu Thr Pro Ala Gly Pro Asp Ala 1180 1185 1190 1195			17935
35	GTC GCG GTC ACC GCC GTG GAC CCG GCG GGG CCG CCC GTG TTC ACG GCC Val Ala Val Thr Ala Val Asp Pro Ala Gly Arg Pro Val Phe Thr Ala 1200 1205 1210			17983
40	GCC TCG CTC ACC CTG CGA CCG GTC ACG ACC GGG CAG CTG ACC GCG GCC Ala Ser Leu Thr Leu Arg Pro Val Thr Thr Gly Gln Leu Thr Ala Ala 1215 1220 1225			18031
45	GAG GCC GCG CCG GCC CCG CTG TAC CCG GTG CCG TGG ACC GGC CTC CCG Glu Ala Ala Arg Ala Pro Leu Tyr Arg Val Arg Trp Thr Gly Leu Pro 1230 1235 1240			18079
50	GAC ACC GGA ACC GCC CCG GAC CAC ACC TGG CCG GTG GCC GGC GGC CCG Asp Thr Gly Thr Ala Arg Asp His Thr Trp Ala Val Ala Gly Gly Pro 1245 1250 1255			18127
55	GGC GAC CTG TTA CCC GGG GAG ACC CCG CAC CAC CCC GAC CTC GCC TCC Gly Asp Leu Leu Pro Gly Glu Thr Pro His His Pro Asp Leu Ala Ser 1260 1265 1270 1275			18175
60	GCG CTC GCC GAC ACC GCC ACC GCC CCC TTC CCG GTA CTG GCG GAT CTG Ala Leu Ala Asp Thr Gly Thr Ala Pro Phe Arg Val Leu Ala Asp Leu 1280 1285 1290			18223
65	CGC GGA TAC GGC ACC GCC ACC CCC CCG GAA CTC GCC TCC CAG GCG CTC Arg Gly Tyr Gly Thr Ala Thr Pro Arg Glu Leu Ala Ser Gln Ala Leu 1295 1300 1305			18271
70	GCC CTC GTC CAG CAG TGG GCC GAC GCG GCC GAG GCC GCC GAA GGC AGG Ala Leu Val Gln Gln Trp Ala Asp Ala Ala Glu Ala Ala Glu Gly Arg 1310 1315 1320			18319
75	CTC GTC CTG GTG ACA CGC CCG GCC GTC GAC ATC GGT GAC GGC GTC ACG Leu Val Leu Val Thr Arg Arg Ala Val Asp Ile Gly Asp Gly Val Thr 1325 1330 1335			18367

EP 0 791 655 A2

	1325	1330	1335	
5	GAC CCG GCG GCG GCG ACC GTG TGG GGA CTG GTC CGG GCG GCA CAG TCC Asp Pro Ala Ala Ala Thr Val Trp Gly Leu Val Arg Ala Ala Gln Ser 1340 1345 1350 1355	18415		
10	GAG CAC CCC GGG TGC TTC GCG CTC CTC GAC ACC GAC GAC TCC CCC CGC Glu His Pro Gly Cys Phe Ala Leu Leu Asp Thr Asp Asp Ser Pro Arg 1360 1365 1370	18463		
15	TCC CGG CAA CTC CTG CCA CGC GTC GCG GGC ACC GCC GAG CAG CTC GCA Ser Arg Gln Leu Leu Pro Arg Val Ala Gly Thr Ala Glu Gln Leu Ala 1375 1380 1385	18511		
20	CTC CGC GAC GGC ACC CTG CTC GCC CCC TCC CTC ACC CGT GCC ACG CTG Leu Arg Asp Gly Thr Leu Leu Ala Pro Ser Leu Thr Arg Ala Thr Leu 1390 1395 1400	18559		
25	CCC GCC GGC GCC CGG CTG CCC GCA CTC GAC GGC ACC GTC CTG ATC ACT Pro Ala Gly Ala Arg Leu Pro Ala Leu Asp Gly Thr Val Leu Ile Thr 1405 1410 1415	18607		
30	GGG GGC ACC GGC AGC CTC GGC GCG GAG GCG GCC CGC CAT CTG GTC ACC Gly Gly Thr Gly Ser Leu Gly Ala Glu Ala Ala Arg His Leu Val Thr 1420 1425 1430 1435	18655		
35	CGG CAC GGT GCC CGG CGC CTG CTC CTG ACC AGC CGA AGC GGC CGG CAG Arg His Gly Ala Arg Arg Leu Leu Leu Thr Ser Arg Ser Gly Pro Gln 1440 1445 1450	18703		
40	GCC CCC GGC GCG GCC GAA CTC GTC GCC GAA CTG GCC GCC TTG GGC GCC Ala Pro Gly Ala Ala Glu Leu Val Ala Glu Leu Ala Ala Leu Gly Ala 1455 1460 1465	18751		
45	CAC GCG GAC GTG GCC GCC TGC GAC GTC GCC GAC CGC GCC GCC CTG CGG His Ala Asp Val Ala Ala Cys Asp Val Ala Asp Arg Ala Ala Leu Arg 1470 1475 1480	18799		
50	GCC CTG CTC GAC CGC GTA CCC GCC GGC CAC CCG CTG ACC GCG GTC CTG Ala Leu Leu Asp Arg Val Pro Ala Gly His Pro Leu Thr Ala Val Leu 1485 1490 1495	18847		
55	CAC ACG GCG GGC GTC CTG GAC GAC GGC GTC CTC ACC GCC CAG ACA CCG His Thr Ala Gly Val Leu Asp Asp Gly Val Leu Thr Ala Gln Thr Pro 1500 1505 1510 1515	18895		
60	CAG CGG CTC GCG GCC GTC CTC CGC CCG AAG GCC GAC GCC GTA CGC AAT Gln Arg Leu Ala Ala Val Leu Arg Pro Lys Ala Asp Ala Val Arg Asn 1520 1525 1530	18943		
65	CTG CAC GAA CTC ACC CAG GGG CAC GCC CTG TCG GCG TTC ATC CTC TAC Leu His Glu Leu Thr Gln Gly His Ala Leu Ser Ala Phe Ile Leu Tyr 1535 1540 1545	18991		
70	TCG TCG GCC GCC GGA GTG CTC GGC AGC GCG GGC CAG AGC GCC TAC GCC Ser Ser Ala Ala Gly Val Leu Gly Ser Ala Gly Gln Ser Gly Tyr Ala 1550 1555 1560	19039		
75	GCC GCC AAC GCC TAC CTG GAC TCC TTC GCC GTC TGG CGG CGG AGC CGG Ala Ala Asn Ala Tyr Leu Asp Ser Phe Ala Val Trp Arg Arg Ser Arg	19087		

EP 0 791 655 A2

	1565	1570	1575	
5	GGA CTG CCC GCC GTA TCG CTC GGC TGG GGC CCG TGG GAC GGC GGC GGC Gly Leu Pro Ala Val Ser Leu Gly Trp Gly Pro Trp Asp Gly Gly Gly 1580 1585 1590 1595			19135
	ATG GCG AGC GGA CTC GGC GGA ACC GAC ACG GCC CGG CTG CGG CGC AGC Met Ala Ser Gly Leu Gly Gly Thr Asp Thr Ala Arg Leu Arg Arg Ser 1600 1605 1610			19183
10	GGC ATC GCA CCC CTC AGC CGC GCC GAG GGC CTG GCC GCG CTC GAC GCG Gly Ile Ala Pro Leu Ser Arg Ala Glu Gly Leu Ala Ala Leu Asp Ala 1615 1620 1625			19231
15	GCG CTC GCG GCC GGC GGC GAC GAC ACC GCG CCG GCC CAC CTG CTG CCG Ala Leu Ala Ala Gly Gly Asp Asp Thr Ala Pro Ala His Leu Leu Pro 1630 1635 1640			19279
20	ATC CGC GTC GAC GCG GTG ACC CTG CGC GGC GCC GAC ACC GTC CCC GCC Ile Arg Val Asp Ala Val Thr Leu Arg Gly Ala Asp Thr Val Pro Ala 1645 1650 1655			19327
	GTG CTG CGC GAC CTG GCG GGA ACC GCG CCA AGC GCC GCC GAA CGG CCC Val Leu Arg Asp Leu Ala Gly Thr Ala Pro Ser Ala Ala Glu Arg Pro 1660 1665 1670 1675			19375
25	CCC GGG ACA CCG GAG GAC ACG AAC GCG CCC CTG GCG GAC GTC ACC CAA Pro Gly Thr Pro Glu Asp Thr Asn Ala Pro Leu Ala Asp Val Thr Gln 1680 1685 1690			19423
30	CTG CAC GGC CGG GAA CGG AAG GAG GCA CTG ACC GGC TTC GTA CGC GCC Leu His Gly Arg Glu Arg Lys Glu Ala Leu Thr Gly Phe Val Arg Ala 1695 1700 1705			19471
35	CAG GTG GCC GCG GTG CTC GGC CAC CCC ACG TCC GAC ACG ATC GAC GTC Gln Val Ala Ala Val Leu Gly His Pro Thr Ser Asp Thr Ile Asp Val 1710 1715 1720			19519
	CGC CGG AGC TTC AAG GAA GCG GGC TTC GAC TCC CTC ACC GCC GTC GAA Arg Arg Ser Phe Lys Glu Ala Gly Phe Asp Ser Leu Thr Ala Val Glu 1725 1730 1735			19567
40	CTG CGC AAC CGG CTG CGC GCC GCC ACC GGG CTG AAG CTG CCC GCC ACG Leu Arg Asn Arg Leu Arg Ala Ala Thr Gly Leu Lys Leu Pro Ala Thr 1740 1745 1750 1755			19615
45	CTG GTG TTC GAC CAC CCG ACC CCC CTC GCG CTC GCC GGC TTC CTC CAC Leu Val Phe Asp His Pro Thr Pro Leu Ala Leu Ala Gly Phe Leu His 1760 1765 1770			19663
50	CGC GAA CTC CCC GGC GCC GAA GCC TCC CTG ATG AGC GCG ATC GAC ACT Arg Glu Leu Pro Gly Ala Glu Ala Ser Leu Met Ser Ala Ile Asp Thr 1775 1780 1785			19711
	CTC CGG CAC CGG CTG CGC GAC GCC CTG GCC GAC GAC GCC GCA GAC GAC Leu Arg His Arg Leu Arg Asp Ala Leu Ala Asp Asp Ala Ala Asp Asp 1790 1795 1800			19759
55	GCC CTG CGC GAC CAG ATC ACC CGA CGA CTC GAG ACC CTG CTG GCC GGC Ala Leu Arg Asp Gln Ile Thr Arg Arg Leu Glu Thr Leu Leu Ala Gly			19807

EP 0 791 655 A2

	1805	1810	1815	
	ATA GCC CGG ACC GAG GAG CCC GCG CCC GCC ACC GCC GCC GCC GAC GAC			19855
5	Ile Ala Arg Thr Glu Glu Pro Ala Pro Ala Thr Ala Ala Ala Asp Asp			
	1820	1825	1830	1835
	GGG AGC GGA GCC GGT GAT GTC GCG GAA CGA CTG AGC ACC GCG TCG GAC			19903
	Gly Ser Gly Ala Gly Asp Val Ala Glu Arg Leu Ser Thr Ala Ser Asp			
	1840	1845	1850	
10	GAC GAA CTG TTC GAA CTG CTC GAC AGC GGT TTC ACA CCC TGA CCGGCCGGCG			19955
	Asp Glu Leu Phe Glu Leu Leu Asp Ser Gly Phe Thr Pro *			
	1855	1860	1865	
15	GACCGGCACC ACGACATCGA GGCGACCGCA CCGAACACCC CCAGGGGGAA AGCT			20009
	GTG TCC ACC GAG AAC TCC ACC AAC GTC CCG GCG AGC GAG			20048
	Met Ser Thr Glu Asn Ser Thr Asn Val Pro Ala Ser Glu			
	1	5	10	
20	GAC AAG CTC CGC GCC TAT CTG CGT CGC GCG ATG GCC GAC CTC CAC GAG			20096
	Asp Lys Leu Arg Ala Tyr Leu Arg Arg Ala Met Ala Asp Leu His Glu			
	15	20	25	
25	TCC CGC GAA CGG CTC CGC GCC ACG GAA GCG CGC GCC CAG GAG CCG ATC			20144
	Ser Arg Glu Arg Leu Arg Ala Thr Glu Ala Arg Ala Gln Glu Pro Ile			
	30	35	40	45
	GCG GTG GTG GGT ATG GGG TGC CGG TTC CCC GGT GGG GTG GGT TCG CCG			20192
	Ala Val Val Gly Met Gly Cys Arg Phe Pro Gly Gly Val Gly Ser Pro			
	50	55	60	
30	GAG GCG TTG TGG CGG TTG GTG GTG GAG GGG GTG GAC GCG GTT TCC CCG			20240
	Glu Ala Leu Trp Arg Leu Val Val Glu Gly Val Asp Ala Val Ser Pro			
	65	70	75	
35	TTT CCC GGT GAT CGT GGC TGG GAT GTG GAG GGG TTG TAC GAC CCG GAG			20288
	Phe Pro Gly Asp Arg Gly Trp Asp Val Glu Gly Leu Tyr Asp Pro Glu			
	80	85	90	
40	CCG GGT GTG GCG GGG AAG TCG TAT GTG CCG GAG GGG GGT TTT CTG CAT			20336
	Pro Gly Val Ala Gly Lys Ser Tyr Val Arg Glu Gly Gly Phe Leu His			
	95	100	105	
45	GAT GCG GCG GAG TTC GAT GCG GAG TTC TTC GGG ATT TCG CCG CGT GAG			20384
	Asp Ala Ala Glu Phe Asp Ala Glu Phe Phe Gly Ile Ser Pro Arg Glu			
	110	115	120	125
50	GCG GTG GCG ATG GAT CCG CAG CAG CCG CTG TTG CTG GAG ACC TCC TGG			20432
	Ala Val Ala Met Asp Pro Gln Gln Arg Leu Leu Glu Thr Ser Trp			
	130	135	140	
55	GAG GCG ATC GAG CCG GCG GGT ATC GAC CCG CAT TCG CTG CAC GGC AGC			20480
	Glu Ala Ile Glu Arg Ala Gly Ile Asp Pro His Ser Leu His Gly Ser			
	145	150	155	
55	CGC ACC GGC GTC TAC GCC GGC GTG ATG TAC CAC GAC TAT GGC ACG GGA			20528
	Arg Thr Gly Val Tyr Ala Gly Val Met Tyr His Asp Tyr Gly Thr Gly			
	160	165	170	

EP 0 791 655 A2

	CAG ACC TCC GCG ACC GAC ACG AGC GGT TAT TCC GGC ACC GGT ACG TCG Gln Thr Ser Ala Thr Asp Thr Ser Gly Tyr Ser Gly Thr Gly Thr Ser 175 180 185	20576
5	GGG AGT GTG GTG TCG GGG CGT GTG GCC TAC ACG CTG GGG CTG GAG GGT Gly Ser Val Val Ser Gly Arg Val Ala Tyr Thr Leu Gly Leu Glu Gly 190 195 200 205	20624
10	CCG GCC GTG ACC GTG GAT ACG GCG TGT TCG TCG TCG TTG GTG GCG TTG Pro Ala Val Thr Val Asp Thr Ala Cys Ser Ser Ser Leu Val Ala Leu 210 215 220	20672
15	CAT CTG GCG GTG CAG GCG TTG CCG GGT GGC GAG TGT GAC ATG GCG TTG His Leu Ala Val Gln Ala Leu Arg Gly Gly Glu Cys Asp Met Ala Leu 225 230 235	20720
	GCC GGT GGT GTG ACG GTG ATG GCC GGG CCG GGG ATG TTC CTG GAG TTT Ala Gly Gly Val Thr Val Met Ala Gly Pro Gly Met Phe Val Glu Phe 240 245 250	20768
20	TCG CCG CAG CCG GGG TTG GCG GCC GAT GGG CCG TGC AAG GCG TTC GCG Ser Arg Gln Arg Gly Leu Ala Ala Asp Gly Arg Cys Lys Ala Phe Ala 255 260 265	20816
25	GAT GGG GCG GAT GGG ACC GCT TGG GCC GAG GGT GCG GGG GTG GTG CTG Asp Gly Ala Asp Gly Thr Ala Trp Ala Glu Gly Ala Gly Val Val Leu 270 275 280 285	20864
	GTG GAG CCG TTG TCG GAT GCC CCG CCG TTG GGG CAT CCG GTG TTG GCG Val Glu Arg Leu Ser Asp Ala Arg Arg Leu Gly His Pro Val Leu Ala 290 295 300	20912
30	GTG GTG TGT GGG TCG GCG GTG AAT CAG GAC GGT GCG TCG AAT GGT TTG Val Val Cys Gly Ser Ala Val Asn Gln Asp Gly Ala Ser Asn Gly Leu 305 310 315	20960
35	ACG GCG CCG AGT GGT CCG TCG CAG GAG CCG GTG ATT CGT CAG GCG TTG Thr Ala Pro Ser Gly Pro Ser Gln Glu Arg Val Ile Arg Gln Ala Leu 320 325 330	21008
40	GCG AAT GCG CCG TTG ACG GTG GCG GAT GTG GAT GTG GTG GAG GCG CAT Ala Asn Ala Arg Leu Thr Val Ala Asp Val Asp Val Val Glu Ala His 335 340 345	21056
	GGG ACG GGG ACG CCG CTG GGT GAT CCG ATC GAG GCG CAG GCG TTG CTG Gly Thr Gly Thr Arg Leu Gly Asp Pro Ile Glu Ala Gln Ala Leu Leu 350 355 360 365	21104
45	GGG ACG TAT GGG CCG GAT CGT GAT GGT GCG CGT CCG GTG TGG TTG GGG Gly Thr Tyr Gly Arg Asp Arg Asp Gly Gly Arg Pro Val Trp Leu Gly 370 375 380	21152
50	TCG TTG AAG TCG AAT ATT GGT CAT GCT CAG GCG GCT GCG GGG GTG GCT Ser Leu Lys Ser Asn Ile Gly His Ala Gln Ala Ala Ala Gly Val Ala 385 390 395	21200
55	GGT GTG ATC AAG ATG GTG TTG GCG ATG CCG TAT GGG TGG TTG CCG CCG Gly Val Ile Lys Met Val Leu Ala Met Arg Tyr Gly Trp Leu Pro Arg 400 405 410	21248

EP 0 791 655 A2

	ACC TTG CAT GTG GAT GAG CCG AGC CGG CAT GTG GAC TGG TCG GCT GGT	21296
	Thr Leu His Val Asp Glu Pro Ser Arg His Val Asp Trp Ser Ala Gly	
	415 420 425	
5	GGT GTG TGG TTG CTG ACC GAG GCG CGG GAG TGG CCG GGG GTG GAC CGG	21344
	Gly Val Trp Leu Leu Thr Glu Ala Arg Glu Trp Pro Gly Val Asp Arg	
	430 435 440 445	
10	CCG CGT CGG GCG GCG GTC TCC GCC TTT GGT GTC AGT GGT ACC AAC GCC	21392
	Pro Arg Arg Ala Ala Val Ser Ala Phe Gly Val Ser Gly Thr Asn Ala	
	450 455 460	
	CAT CTG ATC CTC GAA GCC CCC GAC ACC GCC GAG GCG GAG AGC GCC ACG	21440
	His Leu Ile Leu Glu Ala Pro Asp Thr Ala Glu Ala Glu Ser Ala Thr	
	465 470 475	
15	ACC CCG GTC CCG TCT GAG GTG TCG GAG TCT GCT GCG GTC TTC GAT GCC	21488
	Thr Pro Val Arg Ser Glu Val Ser Glu Ser Ala Ala Val Phe Asp Ala	
	480 485 490	
20	CGC AGT GGT GTG GTG CCG GTG GTG GTT TCG GGG CGT TCG CCG GTG GTG	21536
	Arg Ser Gly Val Val Pro Val Val Val Ser Gly Arg Ser Arg Val Val	
	495 500 505	
25	GTG CCG GAG GCT CCG GCG CGG TTG GCG GAG GTG GTG GAG GCC GGT GGT	21584
	Val Arg Glu Ala Ala Gly Arg Leu Ala Glu Val Val Glu Ala Gly Gly	
	510 515 520 525	
	GTG GGG CTG GCG GAT GTG GCG GTG ACG ATG GCG GGC CCG TCG CCG TTT	21632
	Val Gly Leu Ala Asp Val Ala Val Thr Met Ala Gly Arg Ser Arg Phe	
	530 535 540	
30	GGG TAT CGG GCG GTT GTG CTG GCT CGG GGT GAG GCT GAG CTT GCC GGG	21680
	Gly Tyr Arg Ala Val Val Leu Ala Arg Gly Glu Ala Glu Leu Ala Gly	
	545 550 555	
35	CGT TTG CGG GCG TTG GCG GGG GGT GAT CCG GAC GCG GGT GTG GTC ACG	21728
	Arg Leu Arg Ala Leu Ala Gly Gly Asp Pro Asp Ala Gly Val Val Thr	
	560 565 570	
40	GGT GCG GTG GTG GAC CCG GAG ACG GCG TCC GGT GGT GGG GGG GTG GTG	21776
	Gly Ala Val Val Asp Pro Glu Thr Gly Ser Gly Gly Gly Gly Val Val	
	575 580 585	
	TTG GTT TTC CCT GGT CAG GGG ACG CAG TGG GTG GGG ATG GGT CCG GGG	21824
	Leu Val Phe Pro Gly Gln Gly Thr Gln Trp Val Gly Met Gly Ala Gly	
	590 595 600 605	
45	CTG CTG GGG TCT TCG GAG GTG TTT GCG GCG TCG ATG CCG GAG TGT GCG	21872
	Leu Leu Gly Ser Ser Glu Val Phe Ala Ser Met Arg Glu Cys Ala	
	610 615 620	
50	CGG GCG CTG AGT GTT CAT GTG GGG TGG GAT TTG CTG GAG GTG GTG TCG	21920
	Arg Ala Leu Ser Val His Val Gly Trp Asp Leu Leu Glu Val Val Ser	
	625 630 635	
55	GGC GGG GCC GGG TTG GAG CCG GTG GAT GTG GTG CAG CCG GTG ACG TGG	21968
	Gly Gly Ala Gly Leu Glu Arg Val Asp Val Val Gln Pro Val Thr Trp	
	640 645 650	

EP 0 791 655 A2

	CCG GTG ATG GTG TCG CTG GCC CGG TAC TGG CAG GCG ATG GGT GTG GAC	22016
	Ala Val Met Val Ser Leu Ala Arg Tyr Trp Gln Ala Met Gly Val Asp	
	655 660 665	
5	GTG GCT GCG GTG GTG GGT CAT TCC CAG GGG GAG ATC GCT GCT GCC ACG	22064
	Val Ala Ala Val Val Gly His Ser Gln Gly Glu Ile Ala Ala Ala Thr	
	670 675 680 685	
10	GTG GCG GGG GCG TTG TCG CTG GAG GAT GCG GCG GCT GTG GTC GCT CTG	22112
	Val Ala Gly Ala Leu Ser Leu Glu Asp Ala Ala Ala Val Val Ala Leu	
	690 695 700	
15	CGG GCG GCG TTG ATT GGC CGG TAT CTG GCG GGT CGT GGT GCG ATG GCG	22160
	Arg Ala Gly Leu Ile Gly Arg Tyr Leu Ala Gly Arg Gly Ala Met Ala	
	705 710 715	
20	GCT GTT CCG CTG CCT GCC GGC GAG GTC GAG GCC GGG CTG GCG AAG TGG	22208
	Ala Val Pro Leu Pro Ala Gly Glu Val Glu Ala Gly Leu Ala Lys Trp	
	720 725 730	
25	CCG GGT GTG GAG GTC GCG GCG GTC AAC GGT CCG GCG TCT ACG GTG GTT	22256
	Pro Gly Val Glu Val Ala Ala Val Asn Gly Pro Ala Ser Thr Val Val	
	735 740 745	
30	TCC GGG GAT CCG CCG GCG GTG GCC GGT TAT GTG GCC GTC TGT CAG GCG	22304
	Ser Gly Asp Arg Arg Ala Val Ala Gly Tyr Val Ala Val Cys Gln Ala	
	750 755 760 765	
35	GAG GGT GTG CAG GCT CCG TTG ATA CCG GTG GAC TAC GCC TCT CAC TCC	22352
	Glu Gly Val Gln Ala Arg Leu Ile Pro Val Asp Tyr Ala Ser His Ser	
	770 775 780	
40	CGC CAT GTG GAG GAC CTG AAG GGC GAG TTG GAG CCG GTG CTG TCC GGT	22400
	Arg His Val Glu Asp Leu Lys Gly Glu Leu Glu Arg Val Leu Ser Gly	
	785 790 795	
45	ATC CGC CCG CGC AGT CCG CCG GTG CCG GTG TGT TCC ACC GTC GCC GGA	22448
	Ile Arg Pro Arg Ser Pro Arg Val Pro Val Cys Ser Thr Val Ala Gly	
	800 805 810	
50	GAG CAG CCG GGC GAG CCG GTT TTC GAT GCG GGG TAT TGG TTC CGT AAT	22496
	Glu Gln Pro Gly Glu Pro Val Phe Asp Ala Gly Tyr Trp Phe Arg Asn	
	815 820 825	
55	CTG CCG AAC CCG GTT GAG TTC TCC GCG GTG GTC GGT GGT TTG TTG GAG	22544
	Leu Arg Asn Arg Val Glu Phe Ser Ala Val Val Gly Gly Leu Leu Glu	
	830 835 840 845	
60	GAG GGC CAC CGT CCG TTC ATC GAG GTC AGT GCC CAC CCG GTA CTC GTT	22592
	Glu Gly His Arg Arg Phe Ile Glu Val Ser Ala His Pro Val Leu Val	
	850 855 860	
65	CAT GCC ATT GAG CAG ACG GCC GAG GCC GCG GAC CCG AGT GTC CAT GCC	22640
	His Ala Ile Glu Gln Thr Ala Glu Ala Ala Asp Arg Ser Val His Ala	
	865 870 875	
70	ACC GGG ACC CTG CGC CGC CAG GAC GAC AGC CCG CAC CGC CTG CTG ACC	22688
	Thr Gly Thr Leu Arg Arg Gln Asp Asp Ser Pro His Arg Leu Leu Thr	
	880 885 890	

EP 0 791 655 A2

	TCC ACC GCC GAG GCC TGG GCC CAC GGC GCC ACC CTC ACC TGG GAC CCC	22736
	Ser Thr Ala Glu Ala Trp Ala His Gly Ala Thr Leu Thr Trp Asp Pro	
	895 900 905	
5	GCC CTG CCC CCA GGC CAC CTC ACC ACC CTC CCC ACC TAC CCC TTC AAC	22784
	Ala Leu Pro Pro Gly His Leu Thr Thr Leu Pro Thr Tyr Pro Phe Asn	
	910 915 920 925	
10	CAC CAC CAC TAC TGG CTC GAC ACC ACC CCC ACC ACC CCC GCG ACG ACC	22832
	His His His Tyr Trp Leu Asp Thr Thr Pro Thr Thr Pro Ala Thr Thr	
	930 935 940	
	ACC CAG AGC CCC ACC GAT GCC CAG AAC CCC GCC GAC GCC CTT CCC TAC	22880
	Thr Gln Ser Pro Thr Asp Ala Gln Asn Pro Ala Asp Ala Leu Pro Tyr	
	945 950 955	
15	AAG GTG AGT TGG AAG CGG TTG CGG GAC CAG GAC AGC TTG ACC GCG CGC	22928
	Lys Val Ser Trp Lys Arg Leu Arg Asp Gln Asp Ser Leu Thr Ala Arg	
	960 965 970	
20	CTC GAC GGC CGA TGG CTG CTG GTG GTA CCG GAG GCG TCG GCG GAC CCG	22976
	Leu Asp Gly Arg Trp Leu Leu Val Val Pro Glu Ala Ser Ala Asp Pro	
	975 980 985	
25	TCG GTT GCT GAG GGC GTC GCG CGC GAG CTG ACC GCG CCG GGC GCG ACC	23024
	Ser Val Ala Glu Gly Val Ala Arg Glu Leu Thr Ala Arg Gly Ala Thr	
	990 995 1000 1005	
	GTG GAG TCG CTG ACG GTC GAG CCG GGC GCC GAC CGT TCG CCG CTG CGC	23072
	Val Glu Ser Leu Thr Val Glu Pro Gly Ala Asp Arg Ser Arg Leu Arg	
	1010 1015 1020	
30	GGG CTG CTG GTC GAC GCC ACG GAA CGG GAC GAA GCC GGG CCG CTG CGC	23120
	Gly Leu Leu Val Asp Ala Thr Glu Arg Asp Glu Ala Gly Pro Leu Arg	
	1025 1030 1035	
35	GGG ATC GTC TCG CTG CTG GCG TTG GCC GGG GAC CAC GCC GGG GCC GAC	23168
	Gly Ile Val Ser Leu Leu Ala Leu Ala Gly Asp His Ala Gly Ala Asp	
	1040 1045 1050	
	GGG GCA CGC CCG GTG GTT CCG GCC GGC CTG GCA GCG TCA CTG GCG CTG	23216
	Gly Ala Arg Pro Val Val Pro Ala Gly Leu Ala Ala Ser Leu Ala Leu	
	1055 1060 1065	
40	ATC CAG GCC GCG GGC GAC GCG GGC ACG GAG GCC GGG CTG TGG GCG GTG	23264
	Ile Gln Ala Ala Gly Asp Ala Gly Thr Glu Ala Gly Leu Trp Ala Val	
	1070 1075 1080 1085	
45	ACC CGC GGC GCC GTC GCG GCC GTG CCC GGT GAC GTA CCG GCG CCG TCG	23312
	Thr Arg Gly Ala Val Ala Val Pro Gly Asp Val Pro Ala Pro Ser	
	1090 1095 1100	
50	CAG GCG CTG CTC TGG GGA TTC GGC CGG GTG GCC GGG ATC GAG CTG CCG	23360
	Gln Ala Leu Leu Trp Gly Phe Gly Arg Val Ala Gly Ile Glu Leu Pro	
	1105 1110 1115	
55	CAC TGC TGG GGC GGC CTG CTC GAC CTG CCG ACC GGG CCC GGC GAC TCC	23408
	His Cys Trp Gly Gly Leu Leu Asp Leu Pro Thr Gly Pro Gly Asp Ser	
	1120 1125 1130	

EP 0 791 655 A2

	GGG TTC CGG CAA CTG GCC GCG ACC CTG GCG GGC CGT CCC GCG GAG GAC	23456
	Gly Phe Arg Gln Leu Ala Ala Thr Leu Ala Gly Arg Pro Ala Glu Asp	
	1135 1140 1145	
5	CAG GTG GCG CTG CGG GCT TCG GGC GCG TAC GGC CGC AGG CTG GTC CGG	23504
	Gln Val Ala Leu Arg Ala Ser Gly Ala Tyr Gly Arg Arg Leu Val Arg	
	1150 1155 1160 1165	
10	GCC TCC GCG GCG GGC GGC GCG GAC GGC TGG CGG CCG CGG GGA ACG GTG	23552
	Ala Ser Ala Ala Gly Gly Ala Asp Gly Trp Arg Pro Arg Gly Thr Val	
	1170 1175 1180	
15	CTG GTG GTG GGC GAC ACC GCG GAG GTC GCC GGA CCG CTG GTG CGC TGG	23600
	Leu Val Val Gly Asp Thr Ala Glu Val Ala Gly Pro Leu Val Arg Trp	
	1185 1190 1195	
20	CTG CTC GGC AAC GGC GCA CGG CGG GTG ACC CTG TCC GGA CTC TCC GGC	23648
	Leu Leu Gly Asn Gly Ala Arg Arg Val Thr Leu Ser Gly Leu Ser Gly	
	1200 1205 1210	
25	CCG CTG CCG GAG GAA CTC GCC GAT GTG GCG GCA CGG GTG ACC GTG GCG	23696
	Pro Leu Pro Glu Glu Leu Ala Asp Val Ala Ala Arg Val Thr Val Ala	
	1215 1220 1225	
30	CCC TGT GAT CCG GCC GAT CGC CCC GCC CTG CGG ACG CTG CTC GCC GAA	23744
	Pro Cys Asp Pro Ala Asp Arg Pro Ala Leu Arg Thr Leu Leu Ala Glu	
	1230 1235 1240 1245	
35	CAG GCG CCG ACC GCC GTG CTC GTG GCG CCC CCG GCC GTC CCG CCC ACG	23792
	Gln Ala Pro Thr Ala Val Leu Val Ala Pro Pro Ala Val Pro Pro Thr	
	1250 1255 1260	
40	CCG CTC GCG GAG ATG ACC GCC GAG GCG TTA GCC ATC GCG CTG TCC GCG	23840
	Pro Leu Ala Glu Met Thr Ala Glu Ala Leu Ala Ile Ala Leu Ser Ala	
	1265 1270 1275	
45	AAG ACC GGT CTG GTC GAC CGT CTG GAC TCG CTG CTC GAC GAG CCG GAC	23888
	Lys Thr Gly Leu Val Asp Arg Leu Asp Ser Leu Leu Asp Glu Pro Asp	
	1280 1285 1290	
50	CCC CTG CTC GAG GAC GGG GAA CTC GAC GCG TTC GTC GTC TTC TCC TCC	23936
	Pro Leu Leu Glu Asp Gly Glu Leu Asp Ala Phe Val Val Phe Ser Ser	
	1295 1300 1305	
55	GTG GCA GGG GTG TGG GGC GGC GCG GGA CAG GGT GGT TAC GCG GCC GGT	23984
	Val Ala Gly Val Trp Gly Gly Ala Gly Gln Gly Gly Tyr Ala Ala Gly	
	1310 1315 1320 1325	
60	ACC GCG TAC CTC GAC GCG CTC GCC GAA TGC CCG CGG GCC GGG GGG CTG	24032
	Thr Ala Tyr Leu Asp Ala Leu Ala Glu Cys Arg Arg Ala Gly Gly Leu	
	1330 1335 1340	
65	CCG GTC ACC TCG GTG GCG TGG ACG CCG TGG CTC GGT ACG CCG GCG GCG	24080
	Pro Val Thr Ser Val Ala Trp Thr Pro Trp Leu Gly Thr Pro Ala Ala	
	1345 1350 1355	
70	GAC TCC CTG GGC GAG CAG ATG AGC CGA GCT GGC ATC ACC CCC CTG GAT	24128
	Asp Ser Leu Gly Glu Gln Met Ser Arg Ala Gly Ile Thr Pro Leu Asp	
	1360 1365 1370	

EP 0 791 655 A2

	CCG GCG GCC TCG CTG GAT GCG CTC GCC CGT GCG GTG GGC CGG CGC GCG	24176
	Pro Ala Ala Ser Leu Asp Ala Leu Ala Arg Ala Val Gly Arg Arg Ala	
	1375 1380 1385	
5	GGC TGT GTG ACG GTC GCC GAC ATC GAC TGG GAG CGG TTC GCC TCC GCG	24224
	Gly Cys Val Thr Val Ala Asp Ile Asp Trp Glu Arg Phe Ala Ser Ala	
	1390 1395 1400 1405	
10	TAC ACG GCC ACC CGT CCC ACG CCG ATG TTC GAC GAG GTG CCC GAG GTG	24272
	Tyr Thr Ala Thr Arg Pro Thr Pro Met Phe Asp Glu Val Pro Glu Val	
	1410 1415 1420	
	CGG CGG ATA CAG GCC GCG TGG GCG GAA GCG GAG GCC GAC GCC GCG CGC	24320
	Arg Arg Ile Gln Ala Ala Trp Ala Glu Ala Glu Ala Asp Ala Ala Arg	
	1425 1430 1435	
15	AGC GGT GCC GGC GGC GAC TCG CAG CTG CTG CGC TCC CTC CGG GGC CGG	24368
	Ser Gly Ala Gly Gly Asp Ser Gln Leu Leu Arg Ser Leu Arg Gly Arg	
	1440 1445 1450	
20	CCC GAG GAG GCC CAA CTG GCG GAG CTG CTG CGG CTG GTG CGC ACC CAT	24416
	Pro Glu Glu Ala Gln Leu Ala Glu Leu Leu Arg Leu Val Arg Thr His	
	1455 1460 1465	
25	GCC GCC GCG GTG CTC GGC CTG GGC TCG CCC GGC GCG GTG GAG GCG CGG	24464
	Ala Ala Ala Val Leu Gly Leu Gly Ser Pro Gly Ala Val Glu Ala Arg	
	1470 1475 1480 1485	
	CGT TCG TTC AAG GAC CTG GGC TTC AAC TCG GTG ACG GCG GTG GAG CTG	24512
	Arg Ser Phe Lys Asp Leu Gly Phe Asn Ser Val Thr Ala Val Glu Leu	
	1490 1495 1500	
30	CGG AAC CGG CTG AAG GAG GCG ACG GGA CTC CGG CTG GAG GTG TCC CTG	24560
	Arg Asn Arg Leu Lys Glu Ala Thr Gly Leu Arg Leu Glu Val Ser Leu	
	1505 1510 1515	
35	GTC TTC GAC CAC CCG GAC CCG GCC TCC CTC GCC CGG CAT CTG CTG GAT	24608
	Val Phe Asp His Pro Asp Pro Ala Ser Leu Ala Arg His Leu Leu Asp	
	1520 1525 1530	
40	CTC GCC CTC GGC CAG GAG CCG GAG GAG ACG CCG CGG GCG TTC GCG CTC	24656
	Leu Ala Leu Gly Gln Glu Pro Glu Glu Thr Pro Arg Ala Phe Ala Leu	
	1535 1540 1545	
	GAA CCC GCG CCG AAC GGG GAG CCG ATC GCG ATC GTG TCC ATG GCC TGC	24704
	Glu Pro Ala Pro Asn Gly Glu Pro Ile Ala Ile Val Ser Met Ala Cys	
	1550 1555 1560 1565	
45	CGT ATG CCG GGG GGT GTC AGC ACG CCC GAG GAG CTG TGG CGG CTG CTG	24752
	Arg Met Pro Gly Gly Val Ser Thr Pro Glu Glu Leu Trp Arg Leu Leu	
	1570 1575 1580	
50	CGG GAC GGC AAG GAC GCG ATC GGG CCG TTC CCC GCC AAC CGG GGC TGG	24800
	Arg Asp Gly Lys Asp Ala Ile Gly Pro Phe Pro Ala Asn Arg Gly Trp	
	1585 1590 1595	
55	GAC CTG GAG AAC CTC TAC GAC CCC GAC CCG GAC GCC GAC GGC CGC ACC	24848
	Asp Leu Glu Asn Leu Tyr Asp Pro Asp Pro Asp Ala Asp Gly Arg Thr	
	1600 1605 1610	

EP 0 791 655 A2

	TAT GTG CGC GAG GGC GGA TTC CTC CAC GAG GCA CCG GAC TTC GAC CCC Tyr Val Arg Glu Gly Gly Phe Leu His Glu Ala Pro Asp Phe Asp Pro 1615 1620 1625	24896
5	TCG TTC TTC GGC ATC TCG CCG CGC GAG GCG CTG GCG ATG GAC CCG CAG Ser Phe Phe Gly Ile Ser Pro Arg Glu Ala Leu Ala Met Asp Pro Gln 1630 1635 1640 1645	24944
10	CAG CGG CTG CTG CTG GAG ACT TCC TGG GAG GCC TTG GAG CGC GCC GGC Gln Arg Leu Leu Leu Glu Thr Ser Trp Glu Ala Leu Glu Arg Ala Gly 1650 1655 1660	24992
	ATC GAC CCG GCG AGG CTG CGC GGC AGC CGT ACC GGC GTC TTC GTC GGC Ile Asp Pro Ala Arg Leu Arg Gly Ser Arg Thr Gly Val Phe Val Gly 1665 1670 1675	25040
15	ACG AAC GGC CAG CAC TAC ATG CCG CTG CTC CAG AAC GGC GGC GAC AGC Thr Asn Gly Gln His Tyr Met Pro Leu Leu Gln Asn Gly Gly Asp Ser 1680 1685 1690	25088
20	TTC GAC GGC TAT CTG GGC ACC GGC AAC TCG GCG AGT GTG ATG TCG GGC Phe Asp Gly Tyr Leu Gly Thr Gly Asn Ser Ala Ser Val Met Ser Gly 1695 1700 1705	25136
25	CGG CTG TCG TAC GTG TTC GGC CTC GAA GGC CCC GCC GTG ACC GTG GAC Arg Leu Ser Tyr Val Phe Gly Leu Glu Gly Pro Ala Val Thr Val Asp 1710 1715 1720 1725	25184
	ACC GCC TGC TCG GCG TCC CTG GTG GCG CTG CAC CTG GCG GTG CAG GCG Thr Ala Cys Ser Ala Ser Leu Val Ala Leu His Leu Ala Val Gln Ala 1730 1735 1740	25232
30	ATG CGG CGC GGC GAG TGC GAC ATG GCG CTG GTC GGC GGC GCG ACG GTG Met Arg Arg Gly Glu Cys Asp Met Ala Leu Val Gly Gly Ala Thr Val 1745 1750 1755	25280
35	ATG TCG ACG CCC GAG ATG CTG GTG GAG TTC TCC CGG CAG CGG GTG ATC Met Ser Thr Pro Glu Met Leu Val Glu Phe Ser Arg Gln Arg Val Ile 1760 1765 1770	25328
	TCC GCC AAC GGC CGG TCG AGG GCC TTC GCC GCC GGT GCC GAC GGT GTG Ser Ala Asn Gly Arg Ser Arg Ala Phe Ala Ala Gly Ala Asp Gly Val 1775 1780 1785	25376
40	GCG CTC GGC GAG GGC GTG GGC GTC CTG CTG GTG GAG CGG CTG TCG GAC Ala Leu Gly Glu Gly Val Gly Val Leu Leu Val Glu Arg Leu Ser Asp 1790 1795 1800 1805	25424
45	GCC GAG CGC AAC GGC CAT CCG GTG CTG GCG GTG GTC CGC GGC TCG GCG Ala Glu Arg Asn Gly His Pro Val Leu Ala Val Val Arg Gly Ser Ala 1810 1815 1820	25472
50	GTC AAC CAG GAC GGC GCC TCC AAC GGG CTG ACG GCG CCC AAC GGG CCC Val Asn Gln Asp Gly Ala Ser Asn Gly Leu Thr Ala Pro Asn Gly Pro 1825 1830 1835	25520
55	TCC CAG CAG CGG GTG ATC CGG CAG GCG CTG GCG GAC GCC GGC CTG CGG Ser Gln Gln Arg Val Ile Arg Gln Ala Leu Ala Asp Ala Gly Leu Arg 1840 1845 1850	25568

EP 0 791 655 A2

	CCC GAG GAC ATC GAC GCC GTC GAG GCG CAC GGC ACC GGC ACC GAG CTG	25616
	Pro Glu Asp Ile Asp Ala Val Glu Ala His Gly Thr Gly Thr Glu Leu	
	1855 1860 1865	
5	GGC GAC CCC ATC GAG GCC GAG GCG CTG CTC GCC ACC TAT GGA AGG ACC	25664
	Gly Asp Pro Ile Glu Ala Glu Ala Leu Leu Ala Thr Tyr Gly Arg Thr	
	1870 1875 1880 1885	
10	CGT ACG GCG GAC CGC CCG CTG TGG CTC GGC TCC CTG AAG TCC AAC ATC	25712
	Arg Thr Ala Asp Arg Pro Leu Trp Leu Gly Ser Leu Lys Ser Asn Ile	
	1890 1895 1900	
	GGG CAC ACC CAG GCC GCC GCC GGC GTG GCG GGC GTC ATC AAG ATG GTG	25760
	Gly His Thr Gln Ala Ala Ala Gly Val Ala Gly Val Ile Lys Met Val	
	1905 1910 1915	
15	CTC GCG CTG GGC AAC GAG ACA CTG CCG CGC ACC CTG CAC GTG GAT GAG	25808
	Leu Ala Leu Gly Asn Glu Thr Leu Pro Arg Thr Leu His Val Asp Glu	
	1920 1925 1930	
20	CCC ACA CCG CGC GTG GAC TGG TCC TCT GGC GCG GTC TCC CTG CTC ACC	25856
	Pro Thr Pro Arg Val Asp Trp Ser Ser Gly Ala Val Ser Leu Leu Thr	
	1935 1940 1945	
25	GAG CCG GTG GAC TGG CCC GCC GGC CCG TCC GCG CCG CGC CGT GCG GCC	25904
	Glu Pro Val Asp Trp Pro Ala Gly Pro Ser Ala Pro Arg Arg Ala Ala	
	1950 1955 1960 1965	
	GTG TCC TCG TTC GGC ATC AGC GGC ACC AAC GCC CAC ACG ATC CTG GAG	25952
	Val Ser Ser Phe Gly Ile Ser Gly Thr Asn Ala His Thr Ile Leu Glu	
	1970 1975 1980	
30	CAG GCC CCC GTC CCC GCG GAG TCC CGC CCC GGG ACG GAG CCG GCG GAC	26000
	Gln Ala Pro Val Pro Ala Glu Ser Arg Pro Gly Thr Glu Pro Ala Asp	
	1985 1990 1995	
35	GGC ACG GGC GCG TGG GAG AAC GTG ACC GTT CCG CTG CTG CTG TCC GGC	26048
	Gly Thr Gly Ala Trp Glu Asn Val Thr Val Pro Leu Leu Ser Gly	
	2000 2005 2010	
	CAC ACC GAG GCG GCG CTG CGC GAG CAG AGC ACG AGG CTG CTG AAC GAC	26096
	His Thr Glu Ala Ala Leu Arg Glu Gln Ser Thr Arg Leu Leu Asn Asp	
	2015 2020 2025	
40	CTG CTG GAG CAC CCG GAC GAG CAC CCG GCC GAC GTC GGC TAC ACC CTG	26144
	Leu Leu Glu His Pro Asp Glu His Pro Ala Asp Val Gly Tyr Thr Leu	
	2030 2035 2040 2045	
45	ATC ACC GGC AGG GCC CAC TTC GGG CAC CCG GCC GCC GTG ATC GGC GAG	26192
	Ile Thr Gly Arg Ala His Phe Gly His Arg Ala Ala Val Ile Gly Glu	
	2050 2055 2060	
50	AGC CCG GAA GAA CTG CTC GAC GCC CTG AAG GCT CTG GCC GAG GGC CGC	26240
	Ser Arg Glu Glu Leu Leu Asp Ala Leu Lys Ala Leu Ala Glu Gly Arg	
	2065 2070 2075	
55	GAG CAC CAC ACC GTG GTA CCG GGC GAC GGG ACG GCC CAC CCG GAC CGC	26288
	Glu His His Thr Val Val Arg Gly Asp Gly Thr Ala His Pro Asp Arg	
	2080 2085 2090	

EP 0 791 655 A2

	CGC GTG GTC TTC GTC TTC CCC GGG CAG GGC TCG CAG TGG CCG TCG ATG	26336
	Arg Val Val Phe Val Phe Pro Gly Gln Gly Ser Gln Trp Pro Ser Met	
	2095 2100 2105	
5	GCC CGG GAC CTG CTC GAC CGC GCG CCC GCC TTC CGC GAG ACG GCG AAG	26384
	Ala Arg Asp Leu Leu Asp Arg Ala Pro Ala Phe Arg Glu Thr Ala Lys	
	2110 2115 2120 2125	
10	GCC TGC GAC GCC GCG CTG AGC GTC CAT CTG GAC TGG TCC GTG CTC GAT	26432
	Ala Cys Asp Ala Ala Leu Ser Val His Leu Asp Trp Ser Val Leu Asp	
	2130 2135 2140	
15	GTC CTC CAG GAG AAG CCG GAC GCG CCG CCG CTG AGC CCG GTC GAC GTG	26480
	Val Leu Gln Glu Lys Pro Asp Ala Pro Pro Leu Ser Arg Val Asp Val	
	2145 2150 2155	
20	GTG CAG CCC GTG CTG TTC ACG ATG ATG CTG TCG CTC GCC GCC TGC TGG	26528
	Val Gln Pro Val Leu Phe Thr Met Met Leu Ser Leu Ala Ala Cys Trp	
	2160 2165 2170	
25	CGG GAC CTC GGC GTC CAC CCG GCC GCC GTG GTG GGC CAC TCC CAG GGA	26576
	Arg Asp Leu Gly Val His Pro Ala Ala Val Val Gly His Ser Gln Gly	
	2175 2180 2185	
30	GAG ATC GCG GCG GCC TGC GTG GCC GGC GCG CTC TCC CTG GAG GAC GCG	26624
	Glu Ile Ala Ala Ala Cys Val Ala Gly Ala Leu Ser Leu Glu Asp Ala	
	2190 2195 2200 2205	
35	GCG CGG ATC GTG GCG CTG CCG AGC CCG GCA TGG CTC ACA CTG GCC GGC	26672
	Ala Arg Ile Val Ala Leu Arg Ser Arg Ala Trp Leu Thr Leu Ala Gly	
	2210 2215 2220	
40	AAG GGC GGC ATG GCC GCC GTC TCC CTG CCG GAA GCC CCG CTG CGC GAG	26720
	Lys Gly Gly Met Ala Ala Val Ser Leu Pro Glu Ala Arg Leu Arg Glu	
	2225 2230 2235	
45	CGG ATC GAG CCG TTC GGG CAG CCG CTG TCG GTG GCC GCG GTG AAC AGC	26768
	Arg Ile Glu Arg Phe Gly Gln Arg Leu Ser Val Ala Ala Val Asn Ser	
	2240 2245 2250	
50	CCG GGC ACG GCG GCG GTC GCC GGT GAC GTG GAC GCG CTG CCG GAA CTG	26816
	Pro Gly Thr Ala Ala Val Ala Gly Asp Val Asp Ala Leu Arg Glu Leu	
	2255 2260 2265	
55	CTG GCG GAG CTG ACC GCG GAG GGC ATC CCG GCC AAG CCG ATC CCC GGC	26864
	Leu Ala Glu Leu Thr Ala Glu Gly Ile Arg Ala Lys Pro Ile Pro Gly	
	2270 2275 2280 2285	
60	GTG GAC ACG GCC GGC CAC TCC GCG CAG GTG GAC GGC CTG AAG GAG CAT	26912
	Val Asp Thr Ala Gly His Ser Ala Gln Val Asp Gly Leu Lys Glu His	
	2290 2295 2300	
65	CTC TTC GAG GTG CTG GCG CCG GTC TCC CCG CCG TCC TCG GAC ATC CCG	26960
	Leu Phe Glu Val Leu Ala Pro Val Ser Pro Arg Ser Ser Asp Ile Pro	
	2305 2310 2315	
70	TTC TAC TCG ACG GTG ACG GGC GCG CCG CTG GAC ACC GAG CCG CTG GAC	27008
	Phe Tyr Ser Thr Val Thr Gly Ala Pro Leu Asp Thr Glu Arg Leu Asp	
	2320 2325 2330	

EP 0 791 655 A2

	GCC GGG TAC TGG TAC CGC AAC ATG CGG GAG CCC GTG GAG TTC GAG AAG	27056
	Ala Gly Tyr Trp Tyr Arg Asn Met Arg Glu Pro Val Glu Phe Glu Lys	
	2335 2340 2345	
5	GCC GTC AGG GCA CTG ATC GCC GAC GGC TAC GAC CTG TTC CTG GAG TGC	27104
	Ala Val Arg Ala Leu Ile Ala Asp Gly Tyr Asp Leu Phe Leu Glu Cys	
	2350 2355 2360 2365	
10	AAC CCG CAC CCG ATG CTC GCC ATG TCG CTG GAC GAG ACA CTC ACC GAC	27152
	Asn Pro His Pro Met Leu Ala Met Ser Leu Asp Glu Thr Leu Thr Asp	
	2370 2375 2380	
15	AGC GGC GGC CAC GGC ACC GTG ATG CAC ACC CTC CGC CGG CAG AAG GGC	27200
	Ser Gly Gly His Gly Thr Val Met His Thr Leu Arg Arg Gln Lys Gly	
	2385 2390 2395	
20	AGC GCC AAG GAC TTC GGC ATG GCG CTC TGC CTC GCC TAT GTC AAC GGA	27248
	Ser Ala Lys Asp Phe Gly Met Ala Leu Cys Leu Ala Tyr Val Asn Gly	
	2400 2405 2410	
25	CTG GAG ATC GAC GGA GAA GCC CTC TTC GGC CCC GAC TCA CGC CGG GTG	27296
	Leu Glu Ile Asp Gly Glu Ala Leu Phe Gly Pro Asp Ser Arg Arg Val	
	2415 2420 2425	
30	AAC CCG CCG ACG TAC CCG TTC CAG CGG GAG CGC TAC TGG TAC CAC CCC	27344
	Asn Pro Pro Thr Tyr Pro Phe Gln Arg Glu Arg Tyr Trp Tyr His Pro	
	2430 2435 2440 2445	
35	ACG AGC GGC AGG CGC GGC GAC ATC ACG GCG GCC GGC GTG GCC GAG GCG	27392
	Thr Ser Gly Arg Arg Gly Asp Ile Thr Ala Ala Gly Val Ala Glu Ala	
	2450 2455 2460	
40	GAG CAC CCG CTG CTC GGC GCC GGC GTC GAA CTC CCG GAG ACC GGG GGC	27440
	Glu His Pro Leu Leu Gly Ala Gly Val Glu Leu Pro Glu Thr Gly Gly	
	2465 2470 2475	
45	ACG GTG TAC ACC GCG CGG TTC GGC CCG GAC AGC CGG CCG TGG CTG GCC	27488
	Thr Val Tyr Thr Ala Arg Phe Gly Pro Asp Ser Arg Pro Trp Leu Ala	
	2480 2485 2490	
50	GAC CAC GCG CTG CTG GGC ACC GTG CTG CTG CCC GGC ACG GCA ATC CTG	27536
	Asp His Ala Leu Leu Gly Thr Val Leu Leu Pro Gly Thr Ala Ile Leu	
	2495 2500 2505	
55	GAC CTG GTG CTG TGG GCG GGC GAA CGC TCC GGC TGC GGC CGC GTC GGT	27584
	Asp Leu Val Leu Trp Ala Gly Glu Arg Ser Gly Cys Gly Arg Val Gly	
	2510 2515 2520 2525	
60	GAA CTG CCG CTC CAG GCA CCG CTG GTC CTG CCG GAC AGC GGC GAC GTC	27632
	Glu Leu Ala Leu Gln Ala Pro Leu Val Leu Pro Asp Ser Gly Asp Val	
	2530 2535 2540	
65	GAA CTG CCG CTG CTG GTC GGC GGC CCG GAC GAG GAG AAA CCG CGC ACC	27680
	Glu Leu Arg Leu Leu Val Gly Gly Pro Asp Glu Glu Lys Arg Arg Thr	
	2545 2550 2555	
70	GTC ACC GTG CAC GCG CGG CCC GCG GCG GCC GGC GCC GAG GCG CCG TGG	27728
	Val Thr Val His Ala Arg Pro Ala Ala Ala Gly Ala Glu Ala Pro Trp	
	2560 2565 2570	

EP 0 791 655 A2

	ACC CGG CAC GCC GAA GCC GTG GTG CTG CCC GCC ACC GGC GAG GAG CCG	27776
	Thr Arg His Ala Glu Ala Val Val Leu Pro Ala Thr Gly Glu Glu Pro	
	2575 2580 2585	
5	ACC CCC GCC CCG CGC CCC GTC CCC GAG CCG GCG GGC ACC ACG GAC CCC	27824
	Thr Pro Ala Pro Arg Pro Val Pro Glu Pro Ala Gly Thr Thr Asp Pro	
	2590 2595 2600 2605	
10	GCC GCG TTC TAC GCG GAG TTC GCC GAG CGC GGC TAC GAC TAC GGC CCG	27872
	Ala Ala Phe Tyr Ala Glu Phe Ala Glu Arg Gly Tyr Asp Tyr Gly Pro	
	2610 2615 2620	
	GCC TTC CAG GGC TTC ACC GCC GGA GCG CGC CAC GGC GAG GAC GTC GTC	27920
	Ala Phe Gln Gly Phe Thr Ala Gly Ala Arg His Gly Glu Asp Val Val	
	2625 2630 2635	
15	GCC GAG GTG GCG CTG CCC AGC GGC CTG GTG GCG GAC GCC CGT CAC CAC	27968
	Ala Glu Val Ala Leu Pro Ser Gly Leu Val Ala Asp Ala Arg His His	
	2640 2645 2650	
20	CGG CTG CAC CCG GCG CTG CTC GAC GCC GCG CTC CAG GCG ATG ATC CTC	28016
	Arg Leu His Pro Ala Leu Leu Asp Ala Ala Leu Gln Ala Met Ile Leu	
	2655 2660 2665	
25	GGC ACG TTC TTT GCC GAC GAC GGC CGC GCC CGG ATG CCG TTC GCG GTG	28064
	Gly Thr Phe Phe Ala Asp Asp Gly Arg Ala Arg Met Pro Phe Ala Val	
	2670 2675 2680 2685	
	CGC GGA GTA CCG CTG CAC ACG GCC GGC GCC GAC CGG CTG CGC GTC CTC	28112
	Arg Gly Val Arg Leu His Thr Ala Gly Ala Asp Arg Leu Arg Val Leu	
	2690 2695 2700	
30	ATC TCC CCG GCG GGC GAC GAG ACC GTA CCG CTG CTC TGC ACC GAC CTC	28160
	Ile Ser Pro Ala Gly Asp Glu Thr Val Arg Leu Leu Cys Thr Asp Leu	
	2705 2710 2715	
35	GCG ACC GGC GCC CCC GTG CTG GAG ATC GAC GAA CTG GTC GTC CGC CCG	28208
	Ala Thr Gly Ala Pro Val Leu Glu Ile Asp Glu Leu Val Val Arg Pro	
	2720 2725 2730	
40	GTG TCC GGC GAG CAG TTG GCG GCC GGC GCC CCG GGC CGC AAC GGC GGC	28256
	Val Ser Gly Glu Gln Leu Ala Ala Gly Ala Pro Gly Arg Asn Gly Gly	
	2735 2740 2745	
	GAG CTG TAC CCG GTC GAC TGG ACG GTG CTG CCG GAG CCC GCC GAG GTG	28304
	Glu Leu Tyr Arg Val Asp Trp Thr Val Leu Pro Glu Pro Ala Glu Val	
	2750 2755 2760 2765	
45	CCC GCG CCG CGC TGG GCC CTC CTC GGC GAG GAC CAC GCC GGC CTG GCC	28352
	Pro Ala Pro Arg Trp Ala Leu Leu Gly Glu Asp His Ala Gly Leu Ala	
	2770 2775 2780	
50	GAT GTG CTC GGA GGG ACG GGC GGC GGC TGC GAG CGG TAC GAC ACC CTC	28400
	Asp Val Leu Gly Gly Thr Gly Gly Gly Cys Glu Arg Tyr Asp Thr Leu	
	2785 2790 2795	
55	ACC GGC CTG CTG GAG GCC ACC ACC CGG TCG GCC GGC GGA ATC CTG CCC	28448
	Thr Gly Leu Leu Glu Ala Thr Thr Arg Ser Ala Gly Gly Ile Leu Pro	
	2800 2805 2810	

EP 0 791 655 A2

	GAC ATC GTC GCG CTC TCC TTG CCC ACC GCC CCG GAG CCC GGC CCC CAG Asp Ile Val Ala Leu Ser Leu Pro Thr Ala Pro Glu Pro Gly Pro Gln 2815 2820 2825	28496
5	GCG GTG CGC GAG GTG CTG TCC CAG GCG CTC GAC GCC GCC CAG GCG TGG Ala Val Arg Glu Val Leu Ser Gln Ala Leu Asp Ala Ala Gln Ala Trp 2830 2835 2840 2845	28544
10	CTG GCC GCC GGC GCC GAG ACC GCC TCC GCC CGG CTG GTG TTC GTC ACC Leu Ala Ala Gly Ala Glu Thr Ala Ser Ala Arg Leu Val Phe Val Thr 2850 2855 2860	28592
15	GGC GGC GCG GTG GCC ACC ACG GCG GAC GAA ACC GTG CGC GAC ATC GCG Gly Gly Ala Val Ala Thr Thr Ala Asp Glu Thr Val Arg Asp Ile Ala 2865 2870 2875	28640
	GCG GCC GCC GTC TGG GGC CTG GTC CGC TCG GCG CAG TCC GAG GAA CCC Ala Ala Ala Val Trp Gly Leu Val Arg Ser Ala Gln Ser Glu Glu Pro 2880 2885 2890	28688
20	GAC CGC ATG GTC CTG CTC GAC CTG GAC GGC GAG CGG CCC ACC GCG CGG Asp Arg Met Val Leu Leu Asp Leu Asp Gly Glu Arg Pro Thr Ala Arg 2895 2900 2905	28736
25	ACG CTG GCG GCG GCG CTC GCG TCC GGC GAA CCG CAA CTC GCC GTG CGC Thr Leu Ala Ala Ala Leu Ala Ser Gly Glu Pro Gln Leu Ala Val Arg 2910 2915 2920 2925	28784
	GGC TCC ACG GTG GCC GCT CCC CGG CTG GCC CCG GCC GGG CCC GGC CCG Gly Ser Thr Val Ala Ala Pro Arg Leu Ala Pro Ala Gly Pro Gly Pro 2930 2935 2940	28832
30	GAG GAC CTC GTA CCG CCC GCC GGC ACC ACC GCC TGG CGG CTC ACC CCC Glu Asp Leu Val Pro Pro Ala Gly Thr Thr Ala Trp Arg Leu Thr Pro 2945 2950 2955	28880
35	GGC GGG GGG ACG CTG GAG GAA CTG TCG CTC GCG CCC GCC CCC GAC GCG Gly Gly Gly Thr Leu Glu Glu Leu Ser Leu Ala Pro Ala Pro Asp Ala 2960 2965 2970	28928
40	GAG GAA CCA CTG GCA CCG GGC CAG GTA CGC ATC GCC GTC CGC GCG GCG Glu Glu Pro Leu Ala Pro Gly Gln Val Arg Ile Ala Val Arg Ala Ala 2975 2980 2985	28976
	GGC GTG AAC TTC CGC GAC GCC CTG ATC GCC CTC GGC ATG TAC CCG GGC Gly Val Asn Phe Arg Asp Ala Leu Ile Ala Leu Gly Met Tyr Pro Gly 2990 2995 3000 3005	29024
45	AAG GGA ACC ATG GGC GCC GAG GGA GCC GGC GTC GTC GTC GAG ACC GCC Lys Gly Thr Met Gly Ala Glu Gly Ala Gly Val Val Val Glu Thr Ala 3010 3015 3020	29072
50	CCC GAT GTC ACC GGC CTC TCC GCC GGA GAC CGC GTG CTC GGC ATG TGG Pro Asp Val Thr Gly Leu Ser Ala Gly Asp Arg Val Leu Gly Met Trp 3025 3030 3035	29120
55	AAC GGC GGC TTC GGG CCC CTC GTG GTG GCC GAC CAC CGC ATG GTG GCC Asn Gly Gly Phe Gly Pro Leu Val Val Ala Asp His Arg Met Val Ala 3040 3045 3050	29168

EP 0 791 655 A2

	CCG ATC CCC CAC GGC TGG TCG TAC GCC GAG GCG GCC TCC GTG CCC GCC	29216
	Pro Ile Pro His Gly Trp Ser Tyr Ala Glu Ala Ala Ser Val Pro Ala	
	3055 3060 3065	
5	GTG CTC CTC ACC TCC TAC TAC GCG CTG ACC CGG CTG GCC CGG GCC CGC	29264
	Val Leu Leu Thr Ser Tyr Tyr Ala Leu Thr Arg Leu Ala Arg Ala Arg	
	3070 3075 3080 3085	
10	ACC GGA CAG ACC GTC CTC GTC CAC GCC GCC GCC GGC GGT GTC GGC ATG	29312
	Thr Gly Gln Thr Val Leu Val His Ala Ala Ala Gly Gly Val Gly Met	
	3090 3095 3100	
	GCG ACC CTC CAA CTC GCC CGC CAC CTC GGC CTG GAG GTG TAC GCC ACC	29360
	Ala Thr Leu Gln Leu Ala Arg His Leu Gly Leu Glu Val Tyr Ala Thr	
	3105 3110 3115	
15	GCG AGC ACC GGC AAA TGG GAC GCC CTG CAG AAG CAC GGC ATC CCC GAC	29408
	Ala Ser Thr Gly Lys Trp Asp Ala Leu Gln Lys His Gly Ile Pro Asp	
	3120 3125 3130	
20	GAC CGC ATC GCC GAC TCC CGC ACC CTG GAC TTC GCC GAG CGC TTC CTG	29456
	Asp Arg Ile Ala Asp Ser Arg Thr Leu Asp Phe Ala Glu Arg Phe Leu	
	3135 3140 3145	
25	TCC CGG ACG GGC GGC CGG GGT GTC GAC ATC GTG CTG AAC TCC CTG GCC	29504
	Ser Arg Thr Gly Gly Arg Gly Val Asp Ile Val Leu Asn Ser Leu Ala	
	3150 3155 3160 3165	
	GCG GAG TTC GTC GAC GCC TCA CTG CGG CTG CTG CCG CGC GGC GGG CAC	29552
	Gly Glu Phe Val Asp Ala Ser Leu Arg Leu Leu Pro Arg Gly Gly His	
	3170 3175 3180	
30	TTC CTG GAA CTC GGC AAG GCC GAC GTC CGC GAC CCC CGG CGG ATC GCC	29600
	Phe Leu Glu Leu Gly Lys Ala Asp Val Arg Asp Pro Arg Arg Ile Ala	
	3185 3190 3195	
35	GCC GCC CAT CCG GGC ACC GAC TAC CGG GCG TTC GAC CTG GTG CAG GCC	29648
	Ala Ala His Pro Gly Thr Asp Tyr Arg Ala Phe Asp Leu Val Gln Ala	
	3200 3205 3210	
40	GGT CCC GAC ACC GTC GGG GAG ATG CTC GGG GAA CTG CTG GAA CTG TTC	29696
	Gly Pro Asp Thr Val Gly Glu Met Leu Gly Glu Leu Leu Glu Leu Phe	
	3215 3220 3225	
	GCG GCC GGA GCG CTG CGC CCG CTG CCG CTC ACC GCC TAC GGC ATA CGC	29744
	Ala Ala Gly Ala Leu Arg Pro Leu Pro Leu Thr Ala Tyr Gly Ile Arg	
	3230 3235 3240 3245	
45	GAC GCC CGC ACC GCC TTG CGC ACC CTC AGC CAG GCC CGG CAC ACC GGC	29792
	Asp Ala Arg Thr Ala Leu Arg Thr Leu Ser Gln Ala Arg His Thr Gly	
	3250 3255 3260	
50	AAG CTC GTG CTG ACG GTG CCT GCC GGA TTC GAC ACC CAC CGC ACG GTG	29840
	Lys Leu Val Leu Thr Val Pro Ala Gly Phe Asp Thr His Arg Thr Val	
	3265 3270 3275	
55	CTC CTC ACC GGC GGC ACG GGC ACG CTC GGC CAG ACA CTC GCC CGC CAT	29888
	Leu Leu Thr Gly Gly Thr Gly Thr Leu Gly Gln Thr Leu Ala Arg His	
	3280 3285 3290	

EP 0 791 655 A2

	CTG GTC AAC CGC CAC GGC GTA CGG CAC CTG CTG CTC GCC GGC CGC ACC	29936
	Leu Val Asn Arg His Gly Val Arg His Leu Leu Leu Ala Gly Arg Thr	
	3295 3300 3305	
5	GGC GCG GCG GCC GAG GGC GTC GCG GAA CTG ATT GGT GAA CTG GGC GAG	29984
	Gly Ala Ala Ala Glu Gly Val Ala Glu Leu Ile Gly Glu Leu Gly Glu	
	3310 3315 3320 3325	
10	TTG GGC GCC GAG GTC CGG GTC GCG GCC TGC GAC GCG GCC GAC CGG CAG	30032
	Leu Gly Ala Glu Val Arg Val Ala Ala Cys Asp Ala Ala Asp Arg Gln	
	3330 3335 3340	
	CGG CTC ACC GAA CTC CTC GCC GGA ATC CCC GTC GAG CAC CCG CTC GGC	30080
	Arg Leu Thr Glu Leu Leu Ala Gly Ile Pro Val Glu His Pro Leu Gly	
	3345 3350 3355	
15	GCC GTC GTC CAC GCC GCG GGC ACC CTC GAC GAC GGC ACC ATC CCC TCA	30128
	Ala Val Val His Ala Ala Gly Thr Leu Asp Asp Gly Thr Ile Pro Ser	
	3360 3365 3370	
20	CTG ACC GGC GAG AAC ATC GAC AAC GTG CTG CGG CCC AAG GCC GAC GCC	30176
	Leu Thr Gly Glu Asn Ile Asp Asn Val Leu Arg Pro Lys Ala Asp Ala	
	3375 3380 3385	
25	GTG CTC AAC CTG CAC GAG CTG ACC CGC GAC GCC GAC CTC TCG GCG TTC	30224
	Val Leu Asn Leu His Glu Leu Thr Arg Asp Ala Asp Leu Ser Ala Phe	
	3390 3395 3400 3405	
	GTC CTC TAC TCG TCC TCC TCG GCG CTG CTC GGC AGC CCC GGC CAG GGC	30272
	Val Leu Tyr Ser Ser Ser Ser Ala Leu Leu Gly Ser Pro Gly Gln Gly	
	3410 3415 3420	
30	GCC TAC GCC GCG GCC AAC GCC TTC CTG GAC GGC TTC GCC CGA TAC CGC	30320
	Ala Tyr Ala Ala Ala Asn Ala Phe Leu Asp Gly Phe Ala Arg Tyr Arg	
	3425 3430 3435	
35	AAG GGC CTC GGG CTG CCG GCG CTC TCG CTG GCC TGG GGA CTG TGG GGC	30368
	Lys Gly Leu Gly Leu Pro Ala Leu Ser Leu Ala Trp Gly Leu Trp Gly	
	3440 3445 3450	
40	AGC AAC AGC CGC ATG GCG GGC CAC CTC GAC CAG TCG GGC ATG CAA CGG	30416
	Ser Asn Ser Arg Met Ala Gly His Leu Asp Gln Ser Gly Met Gln Arg	
	3455 3460 3465	
	CGC CTG AAC CGG AGC GGC ATC ATG GCG CTC ACC GAC GCC GAG GGC CTC	30464
	Arg Leu Asn Arg Ser Gly Ile Met Ala Leu Thr Asp Ala Glu Gly Leu	
	3470 3475 3480 3485	
45	GCC CTG TTC GAC GCC GCA CAG GAC GGC GGG GAC GCG CTG CTG GTG CCG	30512
	Ala Leu Phe Asp Ala Ala Gln Asp Gly Gly Asp Ala Leu Leu Val Pro	
	3490 3495 3500	
50	ATG CGG CTC AAC CGG ACG GCC CTT CGC GCC TCG GGA CGG ATC ACC CCG	30560
	Met Arg Leu Asn Arg Thr Ala Leu Arg Ala Ser Gly Arg Ile Thr Pro	
	3505 3510 3515	
55	TTC CTC AGC GGC TTG GCC GGC GGC GGC CCG GCG GCG GGG GAG AGG CGC	30608
	Phe Leu Ser Gly Leu Ala Gly Gly Gly Pro Ala Ala Gly Glu Arg Arg	
	3520 3525 3530	

EP 0 791 655 A2

	CCC GAG GTG GCA GCC GTA TCC GGG ACA CTC GCG GAA CGG CTG ACC GGG Pro Glu Val Ala Ala Val Ser Gly Thr Leu Ala Glu Arg Leu Thr Gly 3535 3540 3545	30656
5	CTC ACG GCA CAG GAA GGG CAC GCC CTC GTC CTG GCC GAG ATC CGC GCC Leu Thr Ala Gln Glu Gly His Ala Leu Val Leu Ala Glu Ile Arg Ala 3550 3555 3560 3565	30704
10	CAC GCG GCG GCG GTG CTG GGC CAC GGC TCC GAC GAC TCG ATC CCC GAG His Ala Ala Ala Val Leu Gly His Gly Ser Asp Asp Ser Ile Pro Glu 3570 3575 3580	30752
15	GAC CGG GCC TTC AAG GAC CTC GGC TTC GAC TCG CTC ACC GCC GTG GAG Asp Arg Ala Phe Lys Asp Leu Gly Phe Asp Ser Leu Thr Ala Val Glu 3585 3590 3595	30800
	ATG CGC AAC CGG CTG AGC GCG GCC ACC GGC CTC CGG CTG CCC GCC ACC Met Arg Asn Arg Leu Ser Ala Ala Thr Gly Leu Arg Leu Pro Ala Thr 3600 3605 3610	30848
20	CTC GTC TTC GAC CAC CCG ACC CCG GGC GAG CTG GCC GGC CAC CTG AGT Leu Val Phe Asp His Pro Thr Pro Gly Glu Leu Ala Gly His Leu Ser 3615 3620 3625	30896
25	GCT GAA CTG TCC GCC GAC GAT GCC CCG GGC AGC GCC TCC CCG CTT ACC Ala Glu Leu Ser Ala Asp Asp Ala Pro Gly Ser Ala Ser Pro Leu Thr 3630 3635 3640 3645	30944
	GAA CTC GAC CGT TTC GAA GCC CTG TTC ACC GCT CTC GCA CCG GGG ACC Glu Leu Asp Arg Phe Glu Ala Leu Phe Thr Ala Leu Ala Pro Gly Thr 3650 3655 3660	30992
30	ACC AAG GAC ACC CCG GGC GGG GCC GGG GCA CTG ATG ATC GAC GAG GCC Thr Lys Asp Thr Pro Gly Gly Ala Gly Ala Leu Met Ile Asp Glu Ala 3665 3670 3675	31040
35	GAG CGC CAA GAG ATC GCC GGG CGG CTC GCG GCG CTG GCC GGT CTG TGG Glu Arg Gln Glu Ile Ala Gly Arg Leu Ala Ala Leu Ala Gly Leu Trp 3680 3685 3690	31088
40	AAC CGG CTG CAC GGC ACC ACG ACG GCT CCT GAG GAC GGC GAC ACC GTC Asn Arg Leu His Gly Thr Thr Thr Ala Pro Glu Asp Gly Asp Thr Val 3695 3700 3705	31136
	GCG GAC GCC CTG GAA GCC GCG GAC GAC CAC GAG ATC TTC GCA TTC CTC Ala Asp Ala Leu Glu Ala Ala Asp Asp His Glu Ile Phe Ala Phe Leu 3710 3715 3720 3725	31184
45	GAC GAG CGG TTC TGA GCCCGCCCCA GCGACAGCAC AGGTGAAAAC AC ATG GCC Asp Glu Arg Phe * Met Ala 3730 1	31237
50	AAC GCG AAC GAG CAG CAA CTC CGT GCC TAT CTG AAG CGA GCG ACG ACC Asn Ala Asn Glu Gln Gln Leu Arg Ala Tyr Leu Lys Arg Ala Thr Thr 5 10 15	31285
55	GAA CTC CAC CGT ACC TCC GAA CAA CTG AGG GAG GAG CGG GCA CGG GCC Glu Leu His Arg Thr Ser Glu Gln Leu Arg Glu Glu Arg Ala Arg Ala 20 25 30	31333

EP 0 791 655 A2

	CAC GAG CCG ATC GCC GTC GTC GGC ATG GCC TGC CGC TAC CCC GGA GGC	31381
	His Glu Pro Ile Ala Val Val Gly Met Ala Cys Arg Tyr Pro Gly Gly	
	35 40 45 50	
5	GCG AAC ACC CCC GAA CAG TTC TGG GAA CTG CTC GAC ACC GGC ACC GAC	31429
	Ala Asn Thr Pro Glu Gln Phe Trp Glu Leu Leu Asp Thr Gly Thr Asp	
	55 60 65	
10	GCC GCC GCG CCG ATG CCC TCC GAC CGG GGA TGG GAC ACC CAC GGC CTG	31477
	Ala Ala Ala Pro Met Pro Ser Asp Arg Gly Trp Asp Thr His Gly Leu	
	70 75 80	
	TAC GAC CCC GAC CCG GCG GCA GCG GGG CGC ACC TAC TGC CGG GAG GGC	31525
	Tyr Asp Pro Asp Pro Ala Ala Gly Arg Thr Tyr Cys Arg Glu Gly	
	85 90 95	
15	GGC TTC CTC CAC GAC GCG GGC GAC TTC GAC GCG GAC TTC TTC GGC ATT	31573
	Gly Phe Leu His Asp Ala Gly Asp Phe Asp Ala Asp Phe Phe Gly Ile	
	100 105 110	
20	TCG CCG CGT GAG GCG GTG GCG ATG GAT CCG CAG CAG CCG CTG TTG CTG	31621
	Ser Pro Arg Glu Ala Val Ala Met Asp Pro Gln Gln Arg Leu Leu Leu	
	115 120 125 130	
	GAG ACC TCC TGG GAG GCG ATC GAA GCG GCC GGT ATC GAC CCG CGA GGA	31669
	Glu Thr Ser Trp Glu Ala Ile Glu Ala Ala Gly Ile Asp Pro Arg Gly	
	135 140 145	
25	CTC CGC GGC AGC CGC ACC GGG GTG TAC GTG GGC GCC TGG GAC AGC GGC	31717
	Leu Arg Gly Ser Arg Thr Gly Val Tyr Val Gly Ala Trp Asp Ser Gly	
	150 155 160	
30	TAC ACC GGC CAG GCG CAC GCG CCC TCG GCC GAG TTG GAG CCC GAC CTG	31765
	Tyr Thr Gly Gln Ala His Ala Pro Ser Ala Glu Leu Glu Ala Asp Leu	
	165 170 175	
35	CTG ACC GGC GGC GTC GTC AGC TTC ACC TCC GGC CGT ATC GCC TAC ACG	31813
	Leu Thr Gly Gly Val Val Ser Phe Thr Ser Gly Arg Ile Ala Tyr Thr	
	180 185 190	
	CTG GGC CTG GAG GGT CCG GCC TTG ACC GTG GAC ACC GCG TGT TCG TCG	31861
	Leu Gly Leu Glu Gly Pro Ala Leu Thr Val Asp Thr Ala Cys Ser Ser	
	195 200 205 210	
40	TCG CTG GTC GCC CTG CAC AAC GCG GCG CAG GCG CTG CCG CGC GGC GAA	31909
	Ser Leu Val Ala Leu His Asn Ala Ala Gln Ala Leu Arg Arg Gly Glu	
	215 220 225	
45	TGC GAC CTG GCG TTG GCC GGT GGT GTG ACC GTG ATG GCG ACC CCG GCG	31957
	Cys Asp Leu Ala Leu Ala Gly Gly Val Thr Val Met Ala Thr Pro Ala	
	230 235 240	
50	GTG TTC GTC CAG TTC GCC CCG CAG CGA GGG CTG GCG CCG GAC GGC CGC	32005
	Val Phe Val Gln Phe Ala Arg Gln Arg Gly Leu Ala Pro Asp Gly Arg	
	245 250 255	
55	TGC AAG GCG TTC GCC GAC GCC GCC GAC GGC TTC GGC CCC GCC GAG GGT	32053
	Cys Lys Ala Phe Ala Asp Ala Ala Asp Gly Phe Gly Pro Ala Glu Gly	
	260 265 270	

EP 0 791 655 A2

	GTG GGG ATG GTG CTG GTG GAG CGG TTG TCG GAT GCC CGG CGG TTG GGG	32101
	Val Gly Met Val Leu Val Glu Arg Leu Ser Asp Ala Arg Arg Leu Gly	
	275 280 285 290	
5	CAT CCG GTG TTG GCG GTG GTG TGT GGG TCG GCG GTG AAT CAG GAC GGT	32149
	His Pro Val Leu Ala Val Val Cys Gly Ser Ala Val Asn Gln Asp Gly	
	295 300 305	
10	GCG TCG AAT GGT TTG ACG GCG CCG AGT GGT CCG TCG CAG GAG CGG GTG	32197
	Ala Ser Asn Gly Leu Thr Ala Pro Ser Gly Pro Ser Gln Glu Arg Val	
	310 315 320	
	ATT CGT CAG GCG TTG GGG AAT GCG CGG TTG ACG GTG GCG GAT GTG GAT	32245
	Ile Arg Gln Ala Leu Gly Asn Ala Arg Leu Thr Val Ala Asp Val Asp	
	325 330 335	
15	GTG GTG GAG GCG CAT GGG ACG GGG ACG CGG CTG GGT GAT CCG ATC GAG	32293
	Val Val Glu Ala His Gly Thr Gly Thr Arg Leu Gly Asp Pro Ile Glu	
	340 345 350	
20	GCG CAG GCG TTG CTG GGG ACG TAT GGG CGG GAT CGT GAT GGT GGG CGT	32341
	Ala Gln Ala Leu Leu Gly Thr Tyr Gly Arg Asp Arg Asp Gly Gly Arg	
	355 360 365 370	
25	CCG GTG TGG TTG GGG TCG TTG AAG TCG AAT ATT GGT CAT GCT CAG GCG	32389
	Pro Val Trp Leu Gly Ser Leu Lys Ser Asn Ile Gly His Ala Gln Ala	
	375 380 385	
	GCT GCG GGG GTG GCT GGT GTG ATC AAG ATG GTG TTG GCG ATG CGG TAT	32437
	Ala Ala Gly Val Ala Gly Val Ile Lys Met Val Leu Ala Met Arg Tyr	
	390 395 400	
30	GGG TGG TTG CCG CGG ACG TTG CAT GTG GAT GAG CCG AGC CGG CAT GTG	32485
	Gly Trp Leu Pro Arg Thr Leu His Val Asp Glu Pro Ser Arg His Val	
	405 410 415	
35	GAC TGG TCG GCT GGT GGT GTG CGG TTG CTG ACC GAG GCG CGG GAG TGG	32533
	Asp Trp Ser Ala Gly Gly Val Arg Leu Leu Thr Glu Ala Arg Glu Trp	
	420 425 430	
40	CCG GGG GTG GAC CGG CCG CGT CGG GCG GCG GTC TCC GCC TTT GGT GTC	32581
	Pro Gly Val Asp Arg Pro Arg Arg Ala Ala Val Ser Ala Phe Gly Val	
	435 440 445 450	
	AGT GGT ACC AAC GCC CAT CTG ATC CTC GAA GCC CCC GAC ACC GCC GAG	32629
	Ser Gly Thr Asn Ala His Leu Ile Leu Glu Ala Pro Asp Thr Ala Glu	
	455 460 465	
45	GCG GAG AGC GCC ACG ACC CCG GTC CGC TCT GAG GTG TCG GAG TCT GCT	32677
	Ala Glu Ser Ala Thr Thr Pro Val Arg Ser Glu Val Ser Glu Ser Ala	
	470 475 480	
50	GCG GTC CTC GAT GCC CGC AGT GGT GTG GTG CCG GTG GTG GTT TCG GGG	32725
	Ala Val Leu Asp Ala Arg Ser Gly Val Val Pro Val Val Val Ser Gly	
	485 490 495	
55	CGT TCG CGG GTG GTG GTG CGG GAG GCT GCG GGC CGG TTG GCG GAG GTG	32773
	Arg Ser Arg Val Val Val Arg Glu Ala Ala Gly Arg Leu Ala Glu Val	
	500 505 510	

EP 0 791 655 A2

	GTG GAG GCC GGT GGT GTG GGG CTG CCG GAT GTG GCG GTG ACG ATG GCG	32821
	Val Glu Ala Gly Gly Val Gly Leu Ala Asp Val Ala Val Thr Met Ala	
	515 520 525 530	
5	GGC CGG TCG CGG TTT GGG TAT CGG GCG GTT GTG CTG GCT CGG GGT GAG	32869
	Gly Arg Ser Arg Phe Gly Tyr Arg Ala Val Val Leu Ala Arg Gly Glu	
	535 540 545	
10	GCT GAG CTT GCC GGG CGT TTG CCG GCG TTG GCG GGG GGT GAT CCG GAC	32917
	Ala Glu Leu Ala Gly Arg Leu Arg Ala Leu Ala Gly Gly Asp Pro Asp	
	550 555 560	
	CCG GGT GTG GTC ACG GGT CCG GTG GTG GAC CCG GAG ACG GGG TCC GGT	32965
	Ala Gly Val Val Thr Gly Ala Val Val Asp Pro Glu Thr Gly Ser Gly	
	565 570 575	
15	GGT GGG GGG GTG GTG TTG GTT TTC CCT GGT CAG GGG ACG CAG TCG GTG	33013
	Gly Gly Gly Val Val Leu Val Phe Pro Gly Gln Gly Thr Gln Trp Val	
	580 585 590	
20	GGG ATG GGT GCG GGG CTG CTG GGG TCT TCG GAG GTG TTT GCG GCG TCG	33061
	Gly Met Gly Ala Gly Leu Leu Gly Ser Ser Glu Val Phe Ala Ala Ser	
	595 600 605 610	
25	ATG CCG GAG TGT GCG CCG GCG CTG AGT GTT CAT GTG GGG TGG GAT TTG	33109
	Met Arg Glu Cys Ala Arg Ala Leu Ser Val His Val Gly Trp Asp Leu	
	615 620 625	
	CTG GAG GTG GTG TCG GCG GGG GCC GGG TTG GAG CCG GTG GAT GTG GTG	33157
	Leu Glu Val Val Ser Gly Gly Ala Gly Leu Glu Arg Val Asp Val Val	
	630 635 640	
30	CAG CCG GTG ACG TGG GCG GTG ATG GTG TCG CTG GCC CCG TAC TGG CAG	33205
	Gln Pro Val Thr Trp Ala Val Met Val Ser Leu Ala Arg Tyr Trp Gln	
	645 650 655	
35	CCG ATG GGT GTG GAC GTG GCT GCG GTG GTG GGT CAT TCC CAG GGG GAG	33253
	Ala Met Gly Val Asp Val Ala Ala Val Val Gly His Ser Gln Gly Glu	
	660 665 670	
40	ATC GCT GCT GCC ACG GTG GCG GGG GCG TTG TCG CTG GAG GAT GCG GCG	33301
	Ile Ala Ala Ala Thr Val Ala Gly Ala Leu Ser Leu Glu Asp Ala Ala	
	675 680 685 690	
	GCT GTG GTC GCT CTG CCG GCG GGG TTG ATT GGC CCG TAT CTG GCG GGT	33349
	Ala Val Val Ala Leu Arg Ala Gly Leu Ile Gly Arg Tyr Leu Ala Gly	
	695 700 705	
45	CGT GGT CCG ATG GCG GCT GTT CCG CTG CCT GCC GGC GAG GTC GAG GCC	33397
	Arg Gly Ala Met Ala Ala Val Pro Leu Pro Ala Gly Glu Val Glu Ala	
	710 715 720	
50	GGG CTG GCG AAG TGG CCG GGT GTG GAG GTC GCG GCG GTC AAC GGT CCG	33445
	Gly Leu Ala Lys Trp Pro Gly Val Glu Val Ala Ala Val Asn Gly Pro	
	725 730 735	
55	GCG TCT ACG GTG GTT TCC GGG GAT CCG CCG GCG GTG GCC GGT TAT GTG	33493
	Ala Ser Thr Val Val Ser Gly Asp Arg Arg Ala Val Ala Gly Tyr Val	
	740 745 750	

EP 0 791 655 A2

	GCC GTC TGT CAG GCG GAG GGT GTG CAG GCT CGG TTG ATA CCG GTG GAC	33541
	Ala Val Cys Gln Ala Glu Gly Val Gln Ala Arg Leu Ile Pro Val Asp	
	755 760 765 770	
5	TAC GCC TCT CAC TCC CGC CAT GTG GAG GAC CTG AAG GGC GAG TTG GAG	33589
	Tyr Ala Ser His Ser Arg His Val Glu Asp Leu Lys Gly Glu Leu Glu	
	775 780 785	
10	CGG GTG CTG TCC GGT ATC CGC CCC CGC AGT CCG CGG GTG CCG GTG TGT	33637
	Arg Val Leu Ser Gly Ile Arg Pro Arg Ser Pro Arg Val Pro Val Cys	
	790 795 800	
	TCC ACC GTC GCC GGA GAG CAG CCG GGC GAG CCG GTT TTC GAT GCG GGG	33685
	Ser Thr Val Ala Gly Glu Gln Pro Gly Glu Pro Val Phe Asp Ala Gly	
	805 810 815	
15	TAT TGG TTC CGT AAT CTG CGG AAC CGG GTT GAG TTC TCC GCG GTG GTC	33733
	Tyr Trp Phe Arg Asn Leu Arg Asn Arg Val Glu Phe Ser Ala Val Val	
	820 825 830	
20	GGT GGT TTG TTG GAG GAG GGC CAC CGT CGG TTC ATC GAG GTC AGT GCC	33781
	Gly Gly Leu Leu Glu Glu Gly His Arg Arg Phe Ile Glu Val Ser Ala	
	835 840 845 850	
25	CAC CCG GTA CTC GTC CAT GCC ATT GAG CAG ACG GCC GAG GCC GCG GAC	33829
	His Pro Val Leu Val His Ala Ile Glu Gln Thr Ala Glu Ala Ala Asp	
	855 860 865	
	CGG AGT GTC CAT GCC ACC GGG ACC CTG CGC CGC CAG GAC GAC AGC CCG	33877
	Arg Ser Val His Ala Thr Gly Thr Leu Arg Arg Gln Asp Asp Ser Pro	
	870 875 880	
30	CAC CGC CTG CTG ACC TCC ACC GCC GAG GCC TGG GCC CAC GGC GCC ACC	33925
	His Arg Leu Leu Thr Ser Thr Ala Glu Ala Trp Ala His Gly Ala Thr	
	885 890 895	
35	CTC ACC TGG GAC CCC GCC CTG CCC CCA GGC CAC CTC ACC ACC CTC CCC	33973
	Leu Thr Trp Asp Pro Ala Leu Pro Pro Gly His Leu Thr Thr Leu Pro	
	900 905 910	
	ACC TAC CCC TTC AAC CAC CAC CAC TAC TGG CTC GAC ACC ACC CCC ACC	34021
	Thr Tyr Pro Phe Asn His His His Tyr Trp Leu Asp Thr Thr Pro Thr	
	915 920 925 930	
	ACC CCC GCG ACG ACC ACC CAG AGC CCC ACC GAT GCC TGG CGC TAC CGC	34069
	Thr Pro Ala Thr Thr Thr Gln Ser Pro Thr Asp Ala Trp Arg Tyr Arg	
	935 940 945	
45	GTC ACC TGG AAA GCC CTG ACC GAA GAA TCC ACT CCG GCC TCG TCC CCC	34117
	Val Thr Trp Lys Ala Leu Thr Glu Glu Ser Thr Pro Ala Ser Ser Pro	
	950 955 960	
50	TCC GGT CAC TGG CTC CTC GTC ACA CCC CCG ACC CCC GAA GGC CGC ACG	34165
	Ser Gly His Trp Leu Leu Val Thr Pro Pro Thr Pro Glu Gly Arg Thr	
	965 970 975	
55	CTC GGG GAC CGG GCC GCC GGC GCC CTC GCA CGT CAG GGG GCC ACG GTG	34213
	Leu Gly Asp Arg Ala Ala Gly Ala Leu Ala Arg Gln Gly Ala Thr Val	
	980 985 990	

EP 0 791 655 A2

	GAA CGG CTG GTG GTC GAT CCG GTC GCC GTC GGA CGC GAC GGG CTC GCG	34261
	Glu Arg Leu Val Val Asp Pro Val Ala Val Gly Arg Asp Gly Leu Ala	
	995 1000 1005 1010	
5	GCG CGC CTG GGC GAA CGG TGG GAC GGT GTG CTG TCC CTG CTC GGC GCC	34309
	Ala Arg Leu Gly Glu Arg Trp Asp Gly Val Leu Ser Leu Leu Gly Ala	
	1015 1020 1025	
10	GAC GAG CGT CCG CTC CCA CGG CAT CCC GCC CTC AAC CGC GCC GTC ATG	34357
	Asp Glu Arg Pro Leu Pro Arg His Pro Ala Leu Asn Arg Ala Val Met	
	1030 1035 1040	
	GGC ACC ACG CTG CTC GCC CAG GCC GCT CTG GAC GCA GGA TGC GAG GCG	34405
	Gly Thr Thr Leu Leu Ala Gln Ala Ala Leu Asp Ala Gly Cys Glu Ala	
	1045 1050 1055	
15	CGG ATA TGG GCC GTG ACG CGG GAG GCC GTC GCC GTC TCC CCG AGC GAG	34453
	Arg Ile Trp Ala Val Thr Arg Glu Ala Val Ala Val Ser Pro Ser Glu	
	1060 1065 1070	
20	GTG CCG CGG GAC GCC GGC GCG CAG CTC TGG GGG CTC GGG CGG GGC ATC	34501
	Val Pro Arg Asp Ala Gly Ala Gln Leu Trp Gly Leu Gly Arg Gly Ile	
	1075 1080 1085 1090	
	CGG CTG GAA CAC CCC TCC CTC TGG GGC GGA TTG ATC GAT CTG CCC GCC	34549
	Ala Leu Glu His Pro Ser Leu Trp Gly Gly Leu Ile Asp Leu Pro Ala	
25	1095 1100 1105	
	GTG CCG GAC GAA CGC GCG TGG GCC AGG GCC GTC CGG CGG CTC GTC CCG	34597
	Val Pro Asp Glu Arg Ala Trp Ala Arg Ala Val Arg Arg Leu Val Pro	
	1110 1115 1120	
30	CAC GGT GAG GAC CAG ATC GCC GCG CGC GCC TCG GGT GCC TAT GGG CGC	34645
	His Gly Glu Asp Gln Ile Ala Ala Arg Ala Ser Gly Ala Tyr Gly Arg	
	1125 1130 1135	
	AGG CTC CTG CCG GCT CCG CCG GCC GCG TCG CGC CGC ACC TGC ACA CCG	34693
	Arg Leu Leu Pro Ala Pro Pro Ala Ala Ser Arg Arg Thr Cys Thr Pro	
35	1140 1145 1150	
	TCC GGC ACG GTG CTG GTC ACC GGC GGT ACG GGA GCG CTC GGC GGT CAT	34741
	Ser Gly Thr Val Leu Val Thr Gly Gly Thr Gly Ala Leu Gly Gly His	
40	1155 1160 1165 1170	
	CTG GCC CGC CGT CTC GCA CGC GGC GGG ACC GGG CAT CTG GTG CTC ACC	34789
	Leu Ala Arg Arg Leu Ala Arg Gly Gly Thr Gly His Leu Val Leu Thr	
	1175 1180 1185	
45	AGC CGT CGC GGC CCG GAC GCG CCG GGC GCC GGT GAA CTC GCC GGT GAA	34837
	Ser Arg Arg Gly Pro Asp Ala Pro Gly Ala Gly Glu Leu Ala Gly Glu	
	1190 1195 1200	
	CTC GCC TCC CTG GGC GCG AAG GTC ACG GTC GCC GCG TGC GAC ATG GCC	34885
	Leu Ala Ser Leu Gly Ala Lys Val Thr Val Ala Ala Cys Asp Met Ala	
50	1205 1210 1215	
	GAC CGT GAA GCC GTG CGG GCG CTG CTC GAC GAG CAC CGG CCG ACC GCG	34933
	Asp Arg Glu Ala Val Arg Ala Leu Leu Asp Glu His Arg Pro Thr Ala	
55	1220 1225 1230	

EP 0 791 655 A2

	GTG TTC CAC ACG GCG GGC ACG CCC CAC TCG GCG GAG TTC ACG GCG CTG	34981
	Val Phe His Thr Ala Gly Thr Pro His Ser Ala Glu Phe Thr Ala Leu	
	1235 1240 1245 1250	
5	GAC GAG ACG ACG ACG GCC GGG GTG TAC GGC GGG AAG GTC CTG GGT GCC	35029
	Asp Glu Thr Thr Thr Ala Gly Val Tyr Gly Gly Lys Val Leu Gly Ala	
	1255 1260 1265	
10	CGG CAT CTG GAC GAA CTG ACC CGG GAA CTC GGC ATC GGG CTG GAC GCG	35077
	Arg His Leu Asp Glu Leu Thr Arg Glu Leu Gly Ile Gly Leu Asp Ala	
	1270 1275 1280	
	TTC GTC CTC TTC TCC TCC GGC GCC GCG GTC TGG GGC AGC GGC GGC CAG	35125
	Phe Val Leu Phe Ser Ser Gly Ala Ala Val Trp Gly Ser Gly Gly Gln	
	1285 1290 1295	
15	ACC GCT TAC GGG GCC GCG AAC GCC GCG CTG GAC GCC CTC GCC GAG CGG	35173
	Thr Ala Tyr Gly Ala Ala Asn Ala Ala Leu Asp Ala Leu Ala Glu Arg	
	1300 1305 1310	
20	CGC CGT GCC GCC GGG CTG CCC GCG ACC TCC GTC GCC TGG GGC CTG TGG	35221
	Arg Arg Ala Ala Gly Leu Pro Ala Thr Ser Val Ala Trp Gly Leu Trp	
	1315 1320 1325 1330	
25	GGC GGC GGA GGC ATG GGG GAG GGG GAC GGT GAG GAG TTC CTC AGC CGG	35269
	Gly Gly Gly Gly Met Gly Glu Gly Asp Gly Glu Glu Phe Leu Ser Arg	
	1335 1340 1345	
	CGC GGC CTC GGC GTG ATG CCG CCG GAG GAC GCG CTG GAA GCC CTG GAC	35317
	Arg Gly Leu Gly Val Met Pro Pro Glu Asp Ala Leu Glu Ala Leu Asp	
	1350 1355 1360	
30	CGG GCC CTG GAC CGG GAG GAC ACC ACC GTC GTG GTG GCG GAT GTC GAC	35365
	Arg Ala Leu Asp Arg Glu Asp Thr Thr Val Val Val Ala Asp Val Asp	
	1365 1370 1375	
35	TGG GAG CGG TTC GCC CCG GCC TTC ACC GCG TTC CGG CCC AGT GCG CTG	35413
	Trp Glu Arg Phe Ala Pro Ala Phe Thr Ala Phe Arg Pro Ser Ala Leu	
	1380 1385 1390	
	ATC TCC CCG CTG GTC TCG GAC GGC GGG GAG GCC GGG GGG CAG GAC GCC	35461
	Ile Ser Arg Leu Val Ser Asp Gly Gly Glu Ala Gly Gly Gln Asp Ala	
	1395 1400 1405 1410	
40	CCG GAC GGC ACG CTG TTC GCC GCC GGG TTC GCG GCC GCC GGG CCA CTG	35509
	Pro Asp Gly Thr Leu Phe Ala Ala Gly Phe Ala Ala Ala Gly Pro Leu	
	1415 1420 1425	
45	GAG CGG CAG GAG ATG CTG CTC GGC CTG GTG CCG CGG CAT GTG GCC GCC	35557
	Glu Arg Gln Glu Met Leu Leu Gly Leu Val Arg Arg His Val Ala Ala	
	1430 1435 1440	
50	GTA CTC GGC CAC CCG GGG ACC GCG GAC ATC GGT CCC GAC CGT GCT TTC	35605
	Val Leu Gly His Pro Gly Thr Ala Asp Ile Gly Pro Asp Arg Ala Phe	
	1445 1450 1455	
55	AAG GAG CTG GGG TTC AGT TCG GTC ACC GCC GTC GAG CTG GCC GGG CGG	35653
	Lys Glu Leu Gly Phe Ser Ser Val Thr Ala Val Glu Leu Ala Gly Arg	
	1460 1465 1470	

EP 0 791 655 A2

	CTG GGC CGG GAG TGC GGA CGG AAG CTG CCG CCG ACG CTG GTC TTC GAC	35701
	Leu Gly Arg Glu Cys Gly Arg Lys Leu Pro Pro Thr Leu Val Phe Asp	
	1475 1480 1485 1490	
5	CAT CCG ACT GCC GCG GCG GCC GTC GAA CAC CTG GCG GAG CTG CTG ACA	35749
	His Pro Thr Ala Ala Ala Val Glu His Leu Ala Glu Leu Leu Thr	
	1495 1500 1505	
10	CCG CCC GCC GGT CCC GCC GCC GGT CCC CCG GAG GAG GAG GCG CCG GCC	35797
	Pro Pro Ala Gly Pro Ala Ala Gly Pro Arg Glu Glu Glu Ala Arg Ala	
	1510 1515 1520	
	GCC CTG GCG CGC GTG CCG CTC GAA CGG CTG AGG GAA GCC GGC CTG CTG	35845
	Ala Leu Ala Arg Val Pro Leu Glu Arg Leu Arg Glu Ala Gly Leu Leu	
	1525 1530 1535	
15	GAC GCA CTG CTG CCG CTC GCC GCG GAC GAA TCC GGG GCG ACA ACC CCC	35893
	Asp Ala Leu Leu Arg Leu Ala Ala Asp Glu Ser Gly Ala Thr Thr Pro	
	1540 1545 1550	
20	CGT ACG TCT GCC GCG TCC GGC GCA CCC CGC GGC CCG GAG GAG CCG GAC	35941
	Arg Thr Ser Ala Ala Ser Gly Ala Pro Arg Gly Arg Glu Glu Pro Asp	
	1555 1560 1565 1570	
	GGC CGC GGC GAG CCG GAC GGC TCG GGA CAC CGC GAA AGC CCG GAC GCG	35989
25	Gly Arg Gly Glu Pro Asp Gly Ser Gly His Arg Glu Ser Pro Asp Ala	
	1575 1580 1585	
	GCC GGC GGG TCG GAC GCC CTG GAC GAT CTC GAC GGG GAC GCC CTG GTG	36037
	Ala Gly Gly Ser Asp Ala Leu Asp Asp Leu Asp Gly Asp Ala Leu Val	
	1590 1595 1600	
30	CGG CTC GCC CTC GGG GAA CCG GGC GAG TGA CCGCCCGCG GAGCACACCC	36087
	Arg Leu Ala Leu Gly Glu Pro Gly Glu *	
	1605 1610	
35	GGCCGTCTCC GGCCCGGCCG CGGCCGGGCC GGAAGCCATC CGCCGCCAC CCGGTACCGA	36147
	CCCCCAAGC CCTCAAGCC CTTGACCCG TCGATCAGT CAGTCCGCG GTCCTCCACG	36207
	ACCGGTCCGG AATCGCCCCC ACACGAGTCA GGAAGCACAC C ATG GCC ATG TCC	36260
	Met Ala Met Ser	
40	1	
	GCC GAG AGG CTG ACG GAG GCG CTG CCG ACC TCG CTC AAG GAG GCC GAG	36308
	Ala Glu Arg Leu Thr Glu Ala Leu Arg Thr Ser Leu Lys Glu Ala Glu	
	5 10 15 20	
45	CGG CTC CCG CCG CAG AAC CGC GAA CTG AGG GCC GCG CCG GAC GCG GCG	36356
	Arg Leu Arg Arg Gln Asn Arg Glu Leu Arg Ala Ala Arg Asp Ala Ala	
	25 30 35	
50	CGG GAG CCG ATC GCC GTC GTC GGC ATG GCC TGC CGC TAC CCG GGC GGT	36404
	Arg Glu Pro Ile Ala Val Val Gly Met Ala Cys Arg Tyr Pro Gly Gly	
	40 45 50	
55	GTC ACC GGC CCC GAG GAG CTG TGG GAG CTG GTG GCC GGA GGC CCG GAC	36452
	Val Thr Gly Pro Glu Glu Leu Trp Glu Leu Val Ala Gly Gly Arg Asp	
	55 60 65	

EP 0 791 655 A2

	CGC ATC GGG CCG TTC CCC GTG GAC CCG GGC TGG GAC GTG GCG TCG GTG	36500
	Ala Ile Gly Pro Phe Pro Val Asp Arg Gly Trp Asp Val Ala Ser Val	
	70 75 80	
5	TAC GAC CCG GAT CCC GAG TCG AAG GGC ACC ACG TAC TGC CCG GAG GGC	36548
	Tyr Asp Pro Asp Pro Glu Ser Lys Gly Thr Thr Tyr Cys Arg Glu Gly	
	85 90 95 100	
10	GGG TTC CTG GAA GGC GCC GGT GAC TTC GAC GCC GCC TTC TTC GGC ATC	36596
	Gly Phe Leu Glu Gly Ala Gly Asp Phe Asp Ala Ala Phe Phe Gly Ile	
	105 110 115	
15	TCG CCG CCG GAG GCC CTG GTG ATG GAC CCG CAG CAG CCG CTG CTG CTG	36644
	Ser Pro Arg Glu Ala Leu Val Met Asp Pro Gln Gln Arg Leu Leu Leu	
	120 125 130	
20	GAG GTG TCC TGG GAG GCG CTG GAA CCG GCG GGC ATC GAC CCG TCC TCG	36692
	Glu Val Ser Trp Glu Ala Leu Glu Arg Ala Gly Ile Asp Pro Ser Ser	
	135 140 145	
25	CTG CCG GGC AGC CCG GGT GGT GTC TAC GTG GGC GCC GCG CAC GGC TCG	36740
	Leu Arg Gly Ser Arg Gly Gly Val Tyr Val Gly Ala Ala His Gly Ser	
	150 155 160	
30	TAC GCC TCC GAT CCC CCG CTG GTG CCC GAG GGC TCG GAG GGC TAT CTG	36788
	Tyr Ala Ser Asp Pro Arg Leu Val Pro Glu Gly Ser Glu Gly Tyr Leu	
	165 170 175 180	
35	CTG ACC GGC AGC GCC GAC GCG GTG ATG TCC GGC CCG ATC TCC TAC GCG	46836
	Leu Thr Gly Ser Ala Asp Ala Val Met Ser Gly Arg Ile Ser Tyr Ala	
	185 190 195	
40	CTC GGT CTC GAA GGA CCG TCC ATG ACG GTG GAG ACG GCC TGC TCC TCC	36884
	Leu Gly Leu Glu Gly Pro Ser Met Thr Val Glu Thr Ala Cys Ser Ser	
	200 205 210	
45	TCG CTG GTG GCG CTG CAT CTG GCG GTA CCG GCG CTG CCG CAC GGC GAG	36932
	Ser Leu Val Ala Leu His Leu Ala Val Arg Ala Leu Arg His Gly Glu	
	215 220 225	
50	TGC GGG CTC GCG CTG GCG GCC GGG GTG GCG GTG ATG GCC GAT CCG GCC	36980
	Cys Gly Leu Ala Leu Ala Gly Gly Val Ala Val Met Ala Asp Pro Ala	
	230 235 240	
55	GCG TTC GTG GAG TTC TCC CCG CAG AAG GGG CTG GCC GCC GAC GGC CCG	37028
	Ala Phe Val Glu Phe Ser Arg Gln Lys Gly Leu Ala Ala Asp Gly Arg	
	245 250 255 260	
60	TGC AAG GCG TTC TCG GCC GCC GCC GAC GGC ACC GGC TGG GCC GAG GGC	37076
	Cys Lys Ala Phe Ser Ala Ala Ala Asp Gly Thr Gly Trp Ala Glu Gly	
	265 270 275	
65	GTC GGC GTG CTC GTC CTG GAG CCG CTG TCG GAC GCG CCG CCG GCG GGG	37124
	Val Gly Val Leu Val Leu Glu Arg Leu Ser Asp Ala Arg Arg Ala Gly	
	280 285 290	
70	CAC ACG GTC CTC GGC CTG GTC ACC GGC ACC GCG GTC AAC CAG GAC GGT	37172
	His Thr Val Leu Gly Leu Val Thr Gly Thr Ala Val Asn Gln Asp Gly	
	295 300 305	

EP 0 791 655 A2

	GCC TCC AAC GGG CTG ACC GCG CCC AAC GGC CCA GCC CAG CAA CGC GTC	37220
	Ala Ser Asn Gly Leu Thr Ala Pro Asn Gly Pro Ala Gln Gln Arg Val	
	310 315 320	
5	ATC GCC GAG GCG CTC GCC GAC GCC GGG CTG TCC CCG GAG GAC GTG GAC	37268
	Ile Ala Glu Ala Leu Ala Asp Ala Gly Leu Ser Pro Glu Asp Val Asp	
	325 330 335 340	
10	GCG GTC GAG GCG CAC GCC ACC GGC ACC CGG CTC GGC GAC CCC ATC GAG	37316
	Ala Val Glu Ala His Gly Thr Gly Thr Arg Leu Gly Asp Pro Ile Glu	
	345 350 355	
	GCC GGG GCG CTG CTC GCC GCC TCC GGA CGG AAC CGT TCC GGC GAC CAC	37364
	Ala Gly Ala Leu Leu Ala Ala Ser Gly Arg Asn Arg Ser Gly Asp His	
	360 365 370	
15	CCG CTG TGG CTC GGC TCG CTG AAG TCC AAC ATC GGG CAT GCC CAG GCC	37412
	Pro Leu Trp Leu Gly Ser Leu Lys Ser Asn Ile Gly His Ala Gln Ala	
	375 380 385	
20	GCC GCC GGT GTC GGC GGC GTC ATC AAG ATG CTC CAG GCG CTG CGG CAC	37460
	Ala Ala Gly Val Gly Gly Val Ile Lys Met Leu Gln Ala Leu Arg His	
	390 395 400	
25	GGC TTG CTG CCC CGC ACC CTC CAC GCC GAC GAG CCG ACC CCG CAT GCC	37508
	Gly Leu Leu Pro Arg Thr Leu His Ala Asp Glu Pro Thr Pro His Ala	
	405 410 415 420	
	GAC TGG AGC TCC GGC CGG GTA CGG CTG CTC ACC TCC GAG GTG CCG TGG	37556
	Asp Trp Ser Ser Gly Arg Val Arg Leu Leu Thr Ser Glu Val Pro Trp	
	425 430 435	
30	CAG CGG ACC GGC CGG CCC CGG CGG ACC GGG GTG TCC GCC TTC GGC GTC	37604
	Gln Arg Thr Gly Arg Pro Arg Arg Thr Gly Val Ser Ala Phe Gly Val	
	440 445 450	
35	GGC GGC ACC AAT GCC CAT GTC GTC CTC GAA GAG GCA CCC GCC CCG CCC	37652
	Gly Gly Thr Asn Ala His Val Leu Glu Glu Ala Pro Ala Pro Pro	
	455 460 465	
40	GCG CCG GAA CCG GCC GGG GAG GCC CCC GGC GGC TCC CGC GCC GCA GAA	37700
	Ala Pro Glu Pro Ala Gly Glu Ala Pro Gly Gly Ser Arg Ala Ala Glu	
	470 475 480	
	GGG GCG GAA GGG CCC CTG GCC TGG GTG GTC TCC GGA CGC GAC GAG CCG	37748
	Gly Ala Glu Gly Pro Leu Ala Trp Val Val Ser Gly Arg Asp Glu Pro	
	485 490 495 500	
45	GCC CTG CGG TCC CAG GCC CGG CGG CTC CGC GAC CAC CTC TCC CGC ACC	37796
	Ala Leu Arg Ser Gln Ala Arg Arg Leu Arg Asp His Leu Ser Arg Thr	
	505 510 515	
50	CCC GGG GCC CGC CCG CGT GAC ATC GCC TTC TCC CTC GCC GCC ACG CGC	37844
	Pro Gly Ala Arg Pro Arg Asp Ile Ala Phe Ser Leu Ala Ala Thr Arg	
	520 525 530	
55	GCA GCC TTT GAC CAC CGC GCC GTG CTG ATC GGC TCG GAC GGG GCC GAA	37892
	Ala Ala Phe Asp His Arg Ala Val Leu Ile Gly Ser Asp Gly Ala Glu	
	535 540 545	

EP 0 791 655 A2

	CTC	GCC	GCC	GCC	CTG	GAC	GCG	TTG	GCC	GAA	GGA	CGC	GAC	GGT	CCG	GCG	37940
	Leu	Ala	Ala	Ala	Leu	Asp	Ala	Leu	Ala	Glu	Gly	Arg	Asp	Gly	Pro	Ala	
		550					555					560					
5	GTG	GTG	CGC	GGA	GTC	CGC	GAC	CGG	GAC	GGC	AGG	ATG	GCC	TTC	CTC	TTC	37988
	Val	Val	Arg	Gly	Val	Arg	Asp	Arg	Asp	Gly	Arg	Met	Ala	Phe	Leu	Phe	
	565					570					575					580	
10	ACC	GGG	CAG	GGC	AGC	CAG	CGC	GCC	GGG	ATG	GCC	CAC	GAC	CTG	CAT	GCC	38036
	Thr	Gly	Gln	Gly	Ser	Gln	Arg	Ala	Gly	Met	Ala	His	Asp	Leu	His	Ala	
					585					590					595		
15	GCC	CAT	ACC	TTC	TTC	GCG	TCC	GCC	CTC	GAC	GAG	GTG	ACG	GAC	CGT	CTC	38084
	Ala	His	Thr	Phe	Phe	Ala	Ser	Ala	Leu	Asp	Glu	Val	Thr	Asp	Arg	Leu	
				600					605					610			
20	GAC	CCG	CTG	CTC	GGC	CGG	CCG	CTC	GGC	GCG	CTG	CTG	GAC	GCC	CGA	CCC	38132
	Asp	Pro	Leu	Leu	Gly	Arg	Pro	Leu	Gly	Ala	Leu	Leu	Asp	Ala	Arg	Pro	
			615					620					625				
25	GGC	TCG	CCC	GAA	GCG	GCA	CTC	CTG	GAC	CGG	ACC	GAG	TAC	ACC	CAG	CCG	38180
	Gly	Ser	Pro	Glu	Ala	Ala	Leu	Leu	Asp	Arg	Thr	Glu	Tyr	Thr	Gln	Pro	
		630					635					640					
30	GCG	CTC	TTC	GCC	GTC	GAG	GTG	GCG	CTC	CAC	CGG	CTG	CTG	GAG	CAC	TGG	38228
	Ala	Leu	Phe	Ala	Val	Glu	Val	Ala	Leu	His	Arg	Leu	Leu	Glu	His	Trp	
	645					650					655					660	
35	GGG	ATG	CGC	CCC	GAC	CTG	CTG	CTG	GGG	CAC	TCG	GTG	GGC	GAA	CTG	GCG	38276
	Gly	Met	Arg	Pro	Asp	Leu	Leu	Leu	Gly	His	Ser	Val	Gly	Glu	Leu	Ala	
					665					670					675		
40	GCC	GCC	CAC	GTC	GCG	GGT	GTG	CTC	GAT	CTC	GAC	GAC	GCC	TGC	GCG	CTG	38324
	Ala	Ala	His	Val	Ala	Gly	Val	Leu	Asp	Leu	Asp	Asp	Ala	Cys	Ala	Leu	
				680					685					690			
45	GTG	GCC	GCC	CGC	GGC	AGG	CTG	ATG	CAG	CGC	CTG	CCG	CCC	GGC	GGC	GCG	38372
	Val	Ala	Ala	Arg	Gly	Arg	Leu	Met	Gln	Arg	Leu	Pro	Pro	Gly	Gly	Ala	
			695					700					705				
50	ATG	GTC	TCC	GTG	CGG	GCC	GGC	GAG	GAC	GAG	GTC	CGC	GCA	CTG	CTG	GCC	38420
	Met	Val	Ser	Val	Arg	Ala	Gly	Glu	Asp	Glu	Val	Arg	Ala	Leu	Leu	Ala	
		710					715					720					
55	GCG	CGC	GAG	GAC	GCC	GTC	TGC	GTC	GCC	GCG	GTG	AAC	GGC	CCC	CGG	TCG	38468
	Gly	Arg	Glu	Asp	Ala	Val	Cys	Val	Ala	Ala	Val	Asn	Gly	Pro	Arg	Ser	
	725					730					735					740	
60	GTG	GTG	ATC	TCC	GGC	GCG	GAG	GAA	GCG	GTG	GCC	GAG	GCG	GCG	GCG	CAG	38516
	Val	Val	Ile	Ser	Gly	Ala	Glu	Glu	Ala	Val	Ala	Glu	Ala	Ala	Ala	Gln	
					745					750					755		
65	CTC	GCC	GGA	CGA	GGC	CGC	CGC	ACC	AGG	CGG	CTC	CGC	GTC	GCG	CAC	GCC	38564
	Leu	Ala	Gly	Arg	Gly	Arg	Arg	Thr	Arg	Arg	Leu	Arg	Val	Ala	His	Ala	
				760					765					770			
70	TTC	CAC	TCA	CCC	CTG	ATG	GAC	GGC	ATG	CTC	GCC	GGA	TTC	CGG	GAG	GTC	38612
	Phe	His	Ser	Pro	Leu	Met	Asp	Gly	Met	Leu	Ala	Gly	Phe	Arg	Glu	Val	
			775					780					785				

EP 0 791 655 A2

	GCC GCC GGC CTG CGC TAC CGG GAA CCG GAG CTG ACG GTC GTC TCC ACG	38660
	Ala Ala Gly Leu Arg Tyr Arg Glu Pro Glu Leu Thr Val Val Ser Thr	
	790 795 800	
5	GTC ACG GGG CGG CCC GCC CGC CCC GGT GAA CTC ACC GGC CCC GAC TAC	38708
	Val Thr Gly Arg Pro Ala Arg Pro Gly Glu Leu Thr Gly Pro Asp Tyr	
	805 810 815 820	
10	TGG GTG GCC CAG GTC CGT GAG CCC GTG CGC TTC GCG GAC GCG GTC CGC	38756
	Trp Val Ala Gln Val Arg Glu Pro Val Arg Phe Ala Asp Ala Val Arg	
	825 830 835	
	ACG GCA CAC CGC CTC GGA GCC CGC ACC TTC CTG GAG ACC GGC CCG GAC	38804
	Thr Ala His Arg Leu Gly Ala Arg Thr Phe Leu Glu Thr Gly Pro Asp	
	840 845 850	
15	GGC GTG CTG TGC GGC ATG GCA GAG GAG TGC CTG GAG GAC GAC ACC GTG	38852
	Gly Val Leu Cys Gly Met Ala Glu Glu Cys Leu Glu Asp Asp Thr Val	
	855 860 865	
20	GCC CTG CTG CCG GCG ATC CAC AAG CCC GGC ACC GCG CCG CAC GGT CCG	38900
	Ala Leu Leu Pro Ala Ile His Lys Pro Gly Thr Ala Pro His Gly Pro	
	870 875 880	
25	GCG GCT CCC GGC GCG CTG CGG GCG GCC GCC GCC GCG TAC GGC CGG GGC	38948
	Ala Ala Pro Gly Ala Leu Arg Ala Ala Ala Ala Tyr Gly Arg Gly	
	885 890 895 900	
	GCC CGG GTG GAC TGG GCC GGG ATG CAC GCC GAC GGC CCC GAG GGG CCG	38996
	Ala Arg Val Asp Trp Ala Gly Met His Ala Asp Gly Pro Glu Gly Pro	
	905 910 915	
30	GCC CGC CGC GTC GAA CTG CCC GTC CAC GCC TTC CGG CAC CGC CGC TAC	39044
	Ala Arg Arg Val Glu Leu Pro Val His Ala Phe Arg His Arg Arg Tyr	
	920 925 930	
35	TGG CTC GCC CCG GGC CGC GCG GCG GAC ACC GAC GAC TGG ATG TAC CGG	39092
	Trp Leu Ala Pro Gly Arg Ala Ala Asp Thr Asp Asp Trp Met Tyr Arg	
	935 940 945	
	ATC GGC TGG GAC CGG CTG CCG GCT CTG ACC GGC GGG GCC CGG ACC GCC	39140
	Ile Gly Trp Asp Arg Leu Pro Ala Val Thr Gly Gly Ala Arg Thr Ala	
	950 955 960	
40	GGC CGC TGG CTG GTG ATC CAC CCC GAC AGC CCG CGC TGC CGG GAG CTG	39188
	Gly Arg Trp Leu Val Ile His Pro Asp Ser Pro Arg Cys Arg Glu Leu	
	965 970 975 980	
45	TCC GGC CAC GCC GAA CGC GCG CTG CGC GCC GCG GGC GCG AGC CCC GTA	39236
	Ser Gly His Ala Glu Arg Ala Leu Arg Ala Ala Gly Ala Ser Pro Val	
	985 990 995	
50	CCG CTG CCC GTG GAC GCT CCG GCC GCC GAC CGG GCG TCC TTC GCG GCA	39284
	Pro Leu Pro Val Asp Ala Pro Ala Ala Asp Arg Ala Ser Phe Ala Ala	
	1000 1005 1010	
55	CTG CTG CGC TCC GCC ACC GGA CCT GAC ACA CGA GGT GAC ACA GCC GCG	39332
	Leu Leu Arg Ser Ala Thr Gly Pro Asp Thr Arg Gly Asp Thr Ala Ala	
	1015 1020 1025	

EP 0 791 655 A2

	CCC GTG GCC GGT GTG CTG TCG CTG CTG TCC GAG GAG GAT CGG CCC CAT	39380
	Pro Val Ala Gly Val Leu Ser Leu Leu Ser Glu Glu Asp Arg Pro His	
	1030 1035 1040	
5	CGC CAG CAC GCC CCG GTA CCC GCC GGG GTC CTG GCG ACG CTG TCC CTG	39428
	Arg Gln His Ala Pro Val Pro Ala Gly Val Leu Ala Thr Leu Ser Leu	
	1045 1050 1055 1060	
10	ATG CAG GCT ATG GAG GAG GAG GCG GTG GAG GCT CGC GTG TGG TGC GTC	39476
	Met Gln Ala Met Glu Glu Ala Val Glu Ala Arg Val Trp Cys Val	
	1065 1070 1075	
15	TCC CGC GCC GCG GTC GCC GCC GCC GAC CGG GAA CGG CCC GTC GGC GCG	39524
	Ser Arg Ala Ala Val Ala Ala Ala Asp Arg Glu Arg Pro Val Gly Ala	
	1080 1085 1090	
20	GGC GCC GCC CTG TGG GGG CTG GGG CGG GTG GCC GCC CTG GAA CGC CCC	39572
	Gly Ala Ala Leu Trp Gly Leu Gly Arg Val Ala Ala Leu Glu Arg Pro	
	1095 1100 1105	
25	ACC CGG TGG GGC GGT CTC GTG GAC CTG CCC GCC TCG CCC GGT GCG GCG	39620
	Thr Arg Trp Gly Gly Leu Val Asp Leu Pro Ala Ser Pro Gly Ala Ala	
	1110 1115 1120	
30	CAC TGG GCG GCC GCC GTG GAA CGG CTC GCC GGT CCC GAG GAC CAG ATC	39668
	His Trp Ala Ala Ala Val Glu Arg Leu Ala Gly Pro Glu Asp Gln Ile	
	1125 1130 1135 1140	
35	GCC GTG CGC GCG TCC GGC AGT TGG GGC CGG CGC CTC ACC AGG CTG CCG	39716
	Ala Val Arg Ala Ser Gly Ser Trp Gly Arg Arg Leu Thr Arg Leu Pro	
	1145 1150 1155	
40	CGC GAC GGC GGC GGC CGG ACG GCC GCA CCC GCG TAC CGG CCG CGC GGC	39764
	Arg Asp Gly Gly Gly Arg Thr Ala Ala Pro Ala Tyr Arg Pro Arg Gly	
	1160 1165 1170	
45	ACG GTG CTC GTC ACC GGT GGC ACC GGC GCG CTC GGC GGG CAT CTC GCC	39812
	Thr Val Leu Val Thr Gly Gly Thr Gly Ala Leu Gly His Leu Ala	
	1175 1180 1185	
50	CGC TGG CTC GCC GCG GCG GGC GCC GAA CAC CTG GCG CTC ACC AGC CGC	39860
	Arg Trp Leu Ala Ala Ala Gly Ala Glu His Leu Ala Leu Thr Ser Arg	
	1190 1195 1200	
55	CGG GGC CCG GAC GCG CCC GGC GCC GCC GGA CTC GAG GCC GAA CTC CTC	39908
	Arg Gly Pro Asp Ala Pro Gly Ala Ala Gly Leu Glu Ala Glu Leu Leu	
	1205 1210 1215 1220	
60	CTC CTG GGC GCC AAG GTG ACG TTC GCC GCC TGC GAC ACC GCC GAC CGC	39956
	Leu Leu Gly Ala Lys Val Thr Phe Ala Ala Cys Asp Thr Ala Asp Arg	
	1225 1230 1235	
65	GAC GGC CTC GCC CGG GTC CTG CGG GCG ATA CCG GAG GAC ACC CCG CTC	40004
	Asp Gly Leu Ala Arg Val Leu Arg Ala Ile Pro Glu Asp Thr Pro Leu	
	1240 1245 1250	
70	ACC GCG GTG TTC CAC GCC GCG GGC GTA CCG CAG GTC ACG CCG CTG TCC	40052
	Thr Ala Val Phe His Ala Ala Gly Val Pro Gln Val Thr Pro Leu Ser	
	1255 1260 1265	

EP 0 791 655 A2

	CGT ACC TCG CCC GAG CAC TTC GCC GAC GTG TAC GCG GGC AAG GCG GCG Arg Thr Ser Pro Glu His Phe Ala Asp Val Tyr Ala Gly Lys Ala Ala 1270 1275 1280	40100
5	GGC GCC GCG CAC CTG GAC GAA CTG ACC CGC GAA CTC GGC GCC GGA CTC Gly Ala Ala His Leu Asp Glu Leu Thr Arg Glu Leu Gly Ala Gly Leu 1285 1290 1295 1300	40148
10	GAC GCG TTC GTC CTC TAC TCC TCC GGC GCC GGC GTG TGG GGC AGC GCC Asp Ala Phe Val Leu Tyr Ser Ser Gly Ala Gly Val Trp Gly Ser Ala 1305 1310 1315	40196
	GGC CAG GGT GCC TAC GCC GCC GCC AAC GCC GCC CTG GAC GCG CTC GCC Gly Gln Gly Ala Tyr Ala Ala Ala Asn Ala Ala Leu Asp Ala Leu Ala 1320 1325 1330	40244
15	CGG CGC CGT GCG GCG GAC GGA CTC CCC GCC ACC TCC ATC GCC TGG GGC Arg Arg Arg Ala Ala Asp Gly Leu Pro Ala Thr Ser Ile Ala Trp Gly 1335 1340 1345	40292
20	GTG TGG GGC GGC GGC GGT ATG GGG GCC GAC GAG GCG GGC GCG GAG TAT Val Trp Gly Gly Gly Gly Met Gly Ala Asp Glu Ala Gly Ala Glu Tyr 1350 1355 1360	40340
25	CTG GGC CGG CGC GGT ATG CGC CCC ATG GCA CCG GTC TCC GCG CTC CGG Leu Gly Arg Arg Gly Met Arg Pro Met Ala Pro Val Ser Ala Leu Arg 1365 1370 1375 1380	40388
	GCG ATG GCC ACC GCC ATC GCC TCC GGG GAA CCC TGC CCC ACC GTC ACC Ala Met Ala Thr Ala Ile Ala Ser Gly Glu Pro Cys Pro Thr Val Thr 1385 1390 1395	40436
30	CAC ACC GAC TGG GAG CGC TTC GGC GAG GGC TTC ACC GCC TTC CGG CCC His Thr Asp Trp Glu Arg Phe Gly Glu Gly Phe Thr Ala Phe Arg Pro 1400 1405 1410	40484
35	AGC CCT CTG ATC GCG GGG CTC GGC ACG CCG GGC GGC GGC CGG GCG GCG Ser Pro Leu Ile Ala Gly Leu Gly Thr Pro Gly Gly Gly Arg Ala Ala 1415 1420 1425	40532
	GAG ACC CCC GAG GAG GGG AAC GCC ACC GCT GCG GCG GAC CTC ACC GCC Glu Thr Pro Glu Glu Gly Asn Ala Thr Ala Ala Ala Asp Leu Thr Ala 1430 1435 1440	40580
40	CTG CCG CCC GCC GAA CTC CGC ACC GCG CTG CGC GAG CTG GTG CGA GCC Leu Pro Pro Ala Glu Leu Arg Thr Ala Leu Arg Glu Leu Val Arg Ala 1445 1450 1455 1460	40628
45	CGG ACC GCC GCG GCG CTC GGC CTC GAC GAT CCG GCC GAG GTC GCC GAG Arg Thr Ala Ala Ala Leu Gly Leu Asp Asp Pro Ala Glu Val Ala Glu 1465 1470 1475	40676
50	GGC GAA CGG TTC CCC GCC ATG GGC TTC GAC TCC CTG GCC ACC GTA CGG Gly Glu Arg Phe Pro Ala Met Gly Phe Asp Ser Leu Ala Thr Val Arg 1480 1485 1490	40724
55	CTG CGC CGC GGA CTC GCC TCG GCC ACG GGC CTC GAC CTG CCC CCC GAT Leu Arg Arg Gly Leu Ala Ser Ala Thr Gly Leu Asp Leu Pro Pro Asp 1495 1500 1505	40772

EP 0 791 655 A2

	CTG CTC TTC GAC CGG GAC ACC CCG GCC GCG CTC GCC GCC CAC CTG GCC Leu Leu Phe Asp Arg Asp Thr Pro Ala Ala Leu Ala Ala His Leu Ala 1510 1515 1520	40820
5	GAA CTG CTC GCC ACC GCA CGG GAC CAC GGA CCC GGC GGC CCC GGG ACC Glu Leu Leu Ala Thr Ala Arg Asp His Gly Pro Gly Gly Pro Gly Thr 1525 1530 1535 1540	40868
10	GGT GCC GCG CCG GCC GAT GCC GGA AGC GGC CTG CCG GCC CTC TAC CGG Gly Ala Ala Pro Ala Asp Ala Gly Ser Gly Leu Pro Ala Leu Tyr Arg 1545 1550 1555	40916
	GAG GCC GTC CGC ACC GGC CGG GCC GCG GAA ATG GCC GAA CTG CTC GCC Glu Ala Val Arg Thr Gly Arg Ala Ala Glu Met Ala Glu Leu Leu Ala 1560 1565 1570	40964
15	GCC GCT TCC CGG TTC CGC CCC GCC TTC GGG ACG GCG GAC CGG CAG CCC Ala Ala Ser Arg Phe Arg Pro Ala Phe Gly Thr Ala Asp Arg Gln Pro 1575 1580 1585	41012
20	GTG GCC CTC GTG CCG CTG GCC GAC GGC GCG GAG GAC ACC GGG CTC CCG Val Ala Leu Val Pro Leu Ala Asp Gly Ala Glu Asp Thr Gly Leu Pro 1590 1595 1600	41060
25	CTG CTC GTG GGC TGC GCC GGG ACG GCG GTG GCC TCC GGC CCG GTG GAG Leu Leu Val Gly Cys Ala Gly Thr Ala Val Ala Ser Gly Pro Val Glu 1605 1610 1615 1620	41108
	TTC ACC GCC TTC GCC GGA GCG CTG GCG GAC CTC CCG GCG GCG GCC CCG Phe Thr Ala Phe Ala Gly Ala Leu Ala Asp Leu Pro Ala Ala Ala Pro 1625 1630 1635	41156
30	ATG GCC GCG CTG CCG CAG CCC GGC TTT CTG CCG GGA GAA CGA GTC CCG Met Ala Ala Leu Pro Gln Pro Gly Phe Leu Pro Gly Glu Arg Val Pro 1640 1645 1650	41204
35	GCC ACC CCG GAG GCA TTG TTC GAG GCC CAG GCG GAA GCG CTG CTG CGC Ala Thr Pro Glu Ala Leu Phe Glu Ala Gln Ala Glu Ala Leu Leu Arg 1655 1660 1665	41252
40	TAC GCG GCC GGC CCG CCC TTC GTG CTG CTG GGG CAC TCC GCC GGC GCC Tyr Ala Ala Gly Arg Pro Phe Val Leu Leu Gly His Ser Ala Gly Ala 1670 1675 1680	41300
	AAC ATG GCC CAC GCC CTG ACC CGT CAT CTG GAG GCG AAC GGT GGC GGC Asn Met Ala His Ala Leu Thr Arg His Leu Glu Ala Asn Gly Gly Gly 1685 1690 1695 1700	41348
45	CCC GCA GGG CTG GTG CTC ATG GAC ATC TAC ACC CCC GCC GAC CCC GGC Pro Ala Gly Leu Val Leu Met Asp Ile Tyr Thr Pro Ala Asp Pro Gly 1705 1710 1715	41396
50	GCG ATG GGC GTC TGG CGG AAC GAC ATG TTC CAG TGG GTC TGG CGG CGC Ala Met Gly Val Trp Arg Asn Asp Met Phe Gln Trp Val Trp Arg Arg 1720 1725 1730	41444
55	TCG GAC ATC CCC CCG GAC GAC CAC CGC CTC ACG GCC ATG GGC GCC TAC Ser Asp Ile Pro Pro Asp Asp His Arg Leu Thr Ala Met Gly Ala Tyr 1735 1740 1745	41492

EP 0 791 655 A2

	CAC CGG CTG CTT CTC GAC TGG TCG CCC ACC CCC GTC CGC GCC CCC GTA His Arg Leu Leu Leu Asp Trp Ser Pro Thr Pro Val Arg Ala Pro Val 1750 1755 1760	41540
5	CTG CAT CTG CGC GCC GCG GAA CCC ATG GGC GAC TGG CCA CCC GGG GAC Leu His Leu Arg Ala Ala Glu Pro Met Gly Asp Trp Pro Pro Gly Asp 1765 1770 1775 1780	41588
10	ACC GGC TGG CAG TCC CAC TGG GAC GGC GCG CAC ACC ACC GCC GGC ATC Thr Gly Trp Gln Ser His Trp Asp Gly Ala His Thr Thr Ala Gly Ile 1785 1790 1795	41636
	CCC GGA AAC CAC TTC ACG ATG ATG ACC GAA CAC GCC TCC GCC GCC GCC Pro Gly Asn His Phe Thr Met Met Thr Glu His Ala Ser Ala Ala Ala 1800 1805 1810	41684
15	CGG CTC GTG CAC GGC TGG CTC GCG GAA CGG ACC CCG TCC GGG CAG GGC Arg Leu Val His Gly Trp Leu Ala Glu Arg Thr Pro Ser Gly Gln Gly 1815 1820 1825	41732
20	GGG TCA CCG TCC CGC GCG GCG GGG AGA GAG GAG AGG CCG TGA Gly Ser Pro Ser Arg Ala Ala Gly Arg Glu Glu Arg Pro * 1830 1835 1840	41774
	ACACGGCAGC CGGCCCGACC GGCACCGCCG CCGGCGGCAC CACCGCCCCG GCGGCGGCAC	41834
25	ACGACCTGTC CCGCGCCGGA CGCAGGCTCC AACTCACCCG GGCCGCACAG TGGTTCGCCG	41894
	GCAACCAGGG AGACCCCTAC GGGATGATCC TGCGCGCCGG CACCGCCGAC CCGGCACCGT	41954
	ACGAGGAAGA GATCCGTGAG CGGGGGCCGC TGTTCACAG CGAACTCCTC GCGCCTGGG	42014
30	TGACCGGCAG CCGCCATGTC GCCGACGCCG TGACGGCCGA CGACGCGTTC GGCGCCCTCA	42074
	CCGCGGACGG TGCACGGCCA GGAGTCCGG AACTGCCGCT CTCCGGCAGC GCCCTCGACG	42134
35	CCGCCCACGG GAACCCCGGC GGCCCGCCCC TCCCCGAGG GTGGCCGCAC CGGCCCCCGG	42194
	ACAGGGAGGA GCGAGACGAC CCGACCGGC ACGCGGCGGA CCTGCTGAAC GCCGCCGGCC	42254
	CGGGGCAGGT CCTCGACCTC GTCCCGTTCC CCGGCGGGCT GCGGGCCCCG ACGGCCGGCG	42314
40	CGTGGCTGGG CGTCCCGGCG GAACGGCTGC CGCGCTTCGA GACGGCACTC ACCGGCTGCC	42374
	GCCGCGCCCT CGACGCCCTG CTCTGCCCCC AGCTCCTGGC CGACGCGCGG GCCGGACTGG	42434
	CCGCCGAGGA GGCCCTGCGC GCCGTGCTCG GCGAGACCCC GGAGGCACGC GGACGTCCGC	42494
45	CCGGCGCGGT CGAGGCGGCC CGCGCGCAG CCGTCAGCGC GGCGGAGCCC ATCGCCGTCC	42554
	TGCTGTGCAA CGCGGTGCGG GAACTGATGG AACGGCCGGC CCA GTGGCGG GCGCTCACCG	42614
50	CCGACCCCGG CCTGGCGGGC GCCGCGATCA CCGAAACACT GCTCTGGGCA CCGCCGGTGC	42674
	GCCTGGAGAG CAGGGTGGCA CGCGAGACGG CCGTACTCGC CCGGCGGACG CTGCCCCGTG	42734
	GAACCATCT CGTCGTCTCT GCCGCCGGC CCAACCGCGA CGCCTGCCGG AACGCCGGTC	42794
55	CGGCCGTCAC CGGCTTCGAC GTCTCCGCC GCGCCTCGGA CCGCGGCCCC CAGCCCCACG	42854

EP 0 791 655 A2

GACTCCCCGA GGACCTGCAC TTCCGTCTCT CGGGCCCGCT CGTCCGGCGG ACCGCCGAGG 42914
 CCGGTCTGAG GGCCTCGCC GAACGCTTCC CCGGCTGCGC CCGGCCGGCC CCGCAGTCCG 42974
 5 AGTCCGCCGG TCACCGGTGC TCCGCGGTCT CGGCCGGCTG CCCGTGCCCC CGTATGTCCC 43034
 CGAGTGAGAA GGGCACTGGA TGACCGCCGC CGAGGACCGC ACGGACCGGA AGGGAAACCG 43094
 CCGATGCGCG TACTGCTGAC CTGTATCGCG CACAACACCC ACTACTACAA CCTGGTGCCG 43154
 10 GTCGCCTGGG CCCTGAGAGC GGCCGGACAC GAGGTGCGGG TGGCCGCGCA GCGCCGCCCTC 43214
 ACCGACACGA TCACCGCCTC CGGACTGACC GCCGTGCCGG TCGGCGGCAA CGAGTCCGTG 43274
 CTCGAG 43280

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4473 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ser Ser Ala Leu Arg Arg Ala Val Gln Ser Asn Cys Gly Tyr Gly
 1 5 10 15
 Asp Leu Met Thr Ser Asn Thr Ala Ala Gln Asn Thr Gly Asp Gln Glu
 20 25 30
 Asp Val Asp Gly Pro Asp Ser Thr His Gly Gly Glu Ile Ala Val Val
 35 40 45
 Gly Met Ser Cys Arg Leu Pro Gly Ala Ala Gly Val Glu Glu Phe Trp
 50 55 60
 Glu Leu Leu Arg Ser Gly Arg Gly Met Pro Thr Arg Gln Asp Asp Gly
 65 70 75 80
 Thr Trp Arg Ala Ala Leu Glu Asp His Ala Gly Phe Asp Ala Gly Phe
 85 90 95
 Phe Gly Met Asn Ala Arg Gln Ala Ala Ala Thr Asp Pro Gln His Arg
 100 105 110
 45 Leu Met Leu Glu Leu Gly Trp Glu Ala Leu Glu Asp Ala Gly Ile Val
 115 120 125
 Pro Gly Asp Leu Thr Gly Thr Asp Thr Gly Val Phe Ala Gly Val Ala
 130 135 140
 50 Ser Asp Asp Tyr Ala Val Leu Thr Arg Arg Ser Ala Val Ser Ala Gly
 145 150 155 160
 55 Gly Tyr Thr Ala Thr Gly Leu His Arg Ala Leu Ala Ala Asn Arg Leu
 165 170 175

EP 0 791 655 A2

Ser His Phe Leu Gly Leu Arg Gly Pro Ser Leu Val Val Asp Ser Ala
180 185 190

5 Gln Ser Ala Ser Leu Val Ala Val Gln Leu Ala Cys Glu Ser Leu Arg
195 200 205

Arg Gly Glu Thr Ser Leu Ala Val Ala Gly Gly Val Asn Leu Ile Leu
210 215 220

10 Thr Glu Glu Ser Thr Thr Val Met Glu Arg Met Gly Ala Leu Ser Pro
225 230 235 240

Asp Gly Arg Cys His Thr Phe Asp Ala Arg Ala Asn Gly Tyr Val Arg
245 250 255

15 Gly Glu Gly Gly Gly Ala Val Val Leu Lys Pro Leu Asp Ala Ala Leu
260 265 270

Ala Asp Gly Asp Arg Val Tyr Cys Val Ile Lys Gly Gly Ala Val Asn
275 280 285

20 Asn Asp Gly Gly Gly Ala Ser Leu Thr Thr Pro Asp Arg Glu Ala Gln
290 295 300

Glu Ala Val Leu Arg Gln Ala Tyr Arg Arg Ala Gly Val Ser Thr Gly
305 310 315 320

25 Ala Val Arg Tyr Val Glu Leu His Gly Thr Gly Thr Arg Ala Gly Asp
325 330 335

Pro Val Glu Ala Ala Ala Leu Gly Ala Val Leu Gly Ala Gly Ala Asp
340 345 350

30 Ser Gly Arg Ser Thr Pro Leu Ala Val Gly Ser Val Lys Thr Asn Val
355 360 365

Gly His Leu Glu Gly Ala Ala Gly Ile Val Gly Leu Ile Lys Ala Thr
370 375 380

35 Leu Cys Val Arg Lys Gly Glu Leu Val Pro Ser Leu Asn Phe Ser Thr
385 390 395 400

40 Pro Asn Pro Asp Ile Pro Leu Asp Asp Leu Arg Leu Arg Val Gln Thr
405 410 415

Glu Arg Gln Glu Trp Asn Glu Glu Asp Asp Arg Pro Arg Val Ala Gly
420 425 430

45 Val Ser Ser Phe Gly Met Gly Gly Thr Asn Val His Leu Val Ile Ala
435 440 445

Glu Ala Pro Ala Ala Ala Gly Ser Ser Gly Ala Gly Gly Ser Gly Ala
450 455 460

50 Gly Ser Gly Ala Gly Ile Ser Ala Val Ser Gly Val Val Pro Val Val
465 470 475 480

55 Val Ser Gly Arg Ser Arg Val Val Val Arg Glu Ala Ala Gly Arg Leu
485 490 495

EP 0 791 655 A2

	Ala Glu Val Val Glu Ala Gly Gly Val Gly Leu Ala Asp Val Ala Val	
	500	505 510
5	Thr Met Ala Asp Arg Ser Arg Phe Gly Tyr Arg Ala Val Val Leu Ala	
	515	520 525
	Arg Gly Glu Ala Glu Leu Ala Gly Arg Leu Arg Ala Leu Ala Gly Gly	
	530	535 540
10	Asp Pro Asp Ala Gly Val Val Thr Gly Ala Val Leu Asp Gly Gly Val	
	545	550 555 560
	Val Val Gly Ala Ala Pro Gly Gly Ala Gly Ala Ala Gly Gly Ala Gly	
	565	570 575
15	Ala Ala Gly Gly Ala Gly Gly Gly Gly Val Val Leu Val Phe Pro Gly	
	580	585 590
	Gln Gly Thr Gln Trp Val Gly Met Gly Ala Gly Leu Leu Gly Ser Ser	
	595	600 605
20	Glu Val Phe Ala Ala Ser Met Arg Glu Cys Ala Arg Ala Leu Ser Val	
	610	615 620
	His Val Gly Trp Asp Leu Leu Glu Val Val Ser Gly Gly Ala Gly Leu	
25	625	630 635 640
	Glu Arg Val Asp Val Val Gln Pro Val Thr Trp Ala Val Met Val Ser	
	645	650 655
30	Leu Ala Arg Tyr Trp Gln Ala Met Gly Val Asp Val Ala Ala Val Val	
	660	665 670
	Gly His Ser Gln Gly Glu Ile Ala Ala Ala Thr Val Ala Gly Ala Leu	
	675	680 685
35	Ser Leu Glu Asp Ala Ala Ala Val Val Ala Leu Arg Ala Gly Leu Ile	
	690	695 700
	Gly Arg Tyr Leu Ala Gly Arg Gly Ala Met Ala Ala Val Pro Leu Pro	
	705	710 715 720
40	Ala Gly Glu Val Glu Ala Gly Leu Ala Lys Trp Pro Gly Val Glu Val	
	725	730 735
	Ala Ala Val Asn Gly Pro Ala Ser Thr Val Val Ser Gly Asp Arg Arg	
	740	745 750
45	Ala Val Ala Gly Tyr Val Ala Val Cys Gln Ala Glu Gly Val Gln Ala	
	755	760 765
	Arg Leu Ile Pro Val Asp Tyr Ala Ser His Ser Arg His Val Glu Asp	
50	770	775 780
	Leu Lys Gly Glu Leu Glu Arg Val Leu Ser Gly Ile Arg Pro Arg Ser	
	785	790 795 800
55	Pro Arg Val Pro Val Cys Ser Thr Val Ala Gly Glu Gln Pro Gly Glu	
	805	810 815

EP 0 791 655 A2

Pro Val Phe Asp Ala Gly Tyr Trp Phe Arg Asn Leu Arg Asn Arg Val
820 825 830

5 Glu Phe Ser Ala Val Val Gly Gly Leu Leu Glu Glu Gly His Arg Arg
835 840 845

Phe Ile Glu Val Ser Ala His Pro Val Leu Val His Ala Ile Glu Gln
850 855 860

10 Thr Ala Glu Ala Ala Asp Arg Ser Val His Ala Thr Gly Thr Leu Arg
865 870 875 880

Arg Gln Asp Asp Ser Pro His Arg Leu Leu Thr Ser Thr Ala Glu Ala
885 890 895

15 Trp Ala His Gly Ala Thr Leu Thr Trp Asp Pro Ala Leu Pro Pro Gly
900 905 910

His Leu Thr Thr Leu Pro Thr Tyr Pro Phe Asn His His His Tyr Trp
915 920 925

20 Leu Asp Thr Ile Asp Gly Gly Gly Gly Asp Asp Ala Thr Gln Glu Lys
930 935 940

Glu Ser Gly Pro Leu Thr Arg Glu Leu Arg Gly Leu Pro Ser Ser Gln
945 950 955 960

25 Lys Gln Leu Gly Phe Leu Leu Asp Leu Val Cys Arg His Thr Ala Val
965 970 975

Val Leu Gly Leu Asp Thr Ala Ala Glu Val Asp Pro Asp Leu Ser Phe
980 985 990

30 Lys Lys Gln Gly Ile Gln Ser Met Thr Gly Val Glu Leu Arg Asn Arg
995 1000 1005

Leu Leu Thr Glu Thr Gly Leu Ala Leu Pro Thr Thr Leu Val Tyr Asp
1010 1015 1020

35 Arg Pro Thr Pro Arg Ala Leu Ala Gln Phe Leu His Thr Glu Leu Leu
1025 1030 1035 1040

Asp Gly Ser Pro Ser Gly Ser Val Leu Ala Pro Ala Gln Lys Ser Phe
1045 1050 1055

Glu Ala Gln Glu Pro Ile Ala Val Val Gly Met Gly Cys Arg Phe Pro
1060 1065 1070

45 Gly Gly Val Gly Ser Pro Glu Ala Leu Trp Arg Leu Val Val Glu Gly
1075 1080 1085

Val Asp Ala Val Ser Pro Phe Pro Gly Asp Arg Gly Trp Asp Val Glu
1090 1095 1100

50 Gly Leu Tyr Asp Pro Glu Pro Gly Val Ala Gly Lys Ser Tyr Val Arg
1105 1110 1115 1120

Glu Gly Gly Phe Leu His Asp Ala Ala Glu Phe Asp Ala Glu Phe Phe
1125 1130 1135

55

EP 0 791 655 A2

Gly Ile Ser Pro Arg Glu Ala Val Ala Met Asp Pro Gln Gln Arg Leu
1140 1145 1150

5 Leu Leu Glu Thr Ser Trp Glu Ala Ile Glu Arg Ala Gly Ile Asp Pro
1155 1160 1165

His Ser Leu His Gly Ser Arg Thr Gly Val Tyr Ala Gly Val Met Pro
1170 1175 1180

10 Gln Glu Tyr Gly Pro Arg Leu Ala Glu Gly Ala Glu Gly Ser Asp Gly
1185 1190 1195 1200

Tyr Leu Leu Thr Gly Thr Ser Gly Ser Val Val Ser Gly Arg Val Ala
1205 1210 1215

15 Tyr Thr Leu Gly Leu Glu Gly Pro Ala Val Thr Val Asp Thr Ala Cys
1220 1225 1230

Ser Ser Ser Leu Val Ala Leu His Leu Ala Val Gln Ala Leu Arg Gly
1235 1240 1245

20 Gly Glu Cys Asp Met Ala Leu Ala Gly Gly Val Thr Val Met Ala Gly
1250 1255 1260

Pro Gly Met Phe Val Glu Phe Ser Arg Gln Arg Gly Leu Ala Ala Asp
1265 1270 1275 1280

25 Gly Arg Cys Lys Ala Phe Ala Asp Gly Ala Asp Gly Thr Ala Trp Ala
1285 1290 1295

Glu Gly Ala Gly Val Val Leu Val Glu Arg Leu Ser Asp Ala Arg Arg
1300 1305 1310

30 Leu Gly His Pro Val Leu Ala Val Val Cys Gly Ser Ala Val Asn Gln
1315 1320 1325

35 Asp Gly Ala Ser Asn Gly Leu Thr Ala Pro Ser Gly Pro Ser Gln Glu
1330 1335 1340

Arg Val Ile Arg Gln Ala Leu Gly Asn Ala Arg Leu Thr Val Ala Asp
1345 1350 1355 1360

40 Val Asp Val Val Glu Ala His Gly Thr Gly Thr Arg Leu Gly Asp Pro
1365 1370 1375

Ile Glu Ala Gln Ala Leu Leu Gly Thr Tyr Gly Arg Asp Arg Asp Gly
1380 1385 1390

45 Gly Arg Pro Val Trp Leu Gly Ser Leu Lys Ser Asn Ile Gly His Ala
1395 1400 1405

Gln Ala Ala Ala Gly Val Ala Gly Val Ile Lys Met Val Leu Ala Met
1410 1415 1420

50 Arg Tyr Gly Trp Leu Pro Arg Thr Leu His Val Asp Glu Pro Ser Arg
1425 1430 1435 1440

His Val Asp Trp Ser Ala Gly Gly Val Trp Leu Leu Thr Glu Ala Arg
1445 1450 1455

55

EP 0 791 655 A2

	Glu Trp Pro Gly Val Asp Arg Pro Arg Arg Ala Ala Val Ser Ala Phe	
	1460	1465 1470
5	Gly Val Ser Gly Thr Asn Ala His Leu Ile Leu Glu Ala Pro Asp Thr	
	1475	1480 1485
	Ala Glu Ala Glu Ser Ala Thr Thr Pro Val Arg Ser Glu Val Ser Glu	
	1490	1495 1500
10	Ser Ala Ala Val Leu Asp Ala Arg Ser Gly Val Val Pro Val Val Val	
	1505	1510 1515 1520
	Ser Gly Arg Ser Arg Val Val Val Arg Glu Ala Ala Gly Arg Leu Ala	
	1525	1530 1535
15	Glu Val Val Glu Ala Gly Gly Val Gly Leu Ala Asp Val Ala Val Thr	
	1540	1545 1550
	Met Ala Gly Arg Ser Arg Phe Gly Tyr Arg Ala Val Val Leu Ala Arg	
	1555	1560 1565
20	Gly Glu Ala Glu Leu Ala Gly Arg Leu Arg Ala Leu Ala Gly Gly Asp	
	1570	1575 1580
	Pro Asp Ala Gly Val Val Thr Gly Ala Val Val Asp Pro Glu Thr Gly	
	1585	1590 1595 1600
25	Ser Gly Gly Gly Gly Val Val Leu Val Phe Pro Gly Gln Gly Thr Gln	
	1605	1610 1615
	Trp Val Gly Met Gly Ala Gly Leu Leu Gly Ser Ser Glu Val Phe Ala	
30	1620	1625 1630
	Ala Ser Met Arg Glu Cys Ala Arg Ala Leu Ser Val His Val Glu Trp	
	1635	1640 1645
35	Asp Leu Leu Glu Val Val Ser Gly Gly Ala Gly Leu Glu Arg Val Asp	
	1650	1655 1660
	Val Val Gln Pro Val Thr Trp Ala Val Met Val Ser Leu Ala Arg Tyr	
	1665	1670 1675 1680
40	Trp Gln Ala Met Gly Val Asp Val Ala Ala Val Val Gly His Ser Gln	
	1685	1690 1695
	Gly Glu Ile Ala Ala Ala Thr Val Ala Gly Ala Leu Ser Leu Glu Asp	
	1700	1705 1710
45	Ala Ala Ala Val Val Ala Leu Arg Ala Gly Leu Ile Gly Arg Tyr Leu	
	1715	1720 1725
	Ala Gly Arg Gly Ala Met Ala Ala Val Pro Leu Pro Ala Gly Glu Val	
50	1730	1735 1740
	Glu Ala Gly Leu Ala Lys Trp Pro Gly Val Glu Val Ala Ala Val Asn	
	1745	1750 1755 1760
55	Gly Pro Ala Ser Thr Val Val Ser Gly Asp Arg Arg Ala Val Ala Gly	
	1765	1770 1775

EP 0 791 655 A2

	Tyr Val Ala Val Cys Gln Ala Glu Gly Val Gln Ala Arg Leu Ile Pro	
	1780	1785 1790
5	Val Asp Tyr Ala Ser His Ser Arg His Val Glu Asp Leu Lys Gly Glu	
	1795	1800 1805
	Leu Glu Arg Val Leu Ser Gly Ile Arg Pro Arg Ser Pro Arg Val Pro	
	1810	1815 1820
10	Val Cys Ser Thr Val Ala Gly Glu Gln Pro Gly Glu Pro Val Phe Asp	
	1825	1830 1835 1840
	Ala Gly Tyr Trp Phe Arg Asn Leu Arg Asn Arg Val Glu Phe Ser Ala	
	1845	1850 1855
15	Val Val Gly Gly Leu Leu Glu Glu Gly His Arg Arg Phe Ile Glu Val	
	1860	1865 1870
	Ser Ala His Pro Val Leu Val His Ala Ile Glu Gln Thr Ala Glu Ala	
	1875	1880 1885
20	Ala Asp Arg Ser Val His Ala Thr Gly Thr Leu Arg Arg Gln Asp Asp	
	1890	1895 1900
	Ser Pro His Arg Leu Leu Thr Ser Thr Ala Glu Ala Trp Ala His Gly	
25	1905	1910 1915 1920
	Ala Thr Leu Thr Trp Asp Pro Ala Leu Pro Pro Gly His Leu Thr Thr	
	1925	1930 1935
	Leu Pro Thr Tyr Pro Phe Asn His His His Tyr Trp Leu Asp Thr Thr	
30	1940	1945 1950
	Pro Thr Thr Pro Ala Thr Thr Thr Gln Ser Pro Thr Asp Ala Trp Arg	
	1955	1960 1965
35	Tyr Arg Val Thr Trp Lys Ala Leu Thr Glu Ser Ser Pro Val Arg Pro	
	1970	1975 1980
	His Ser Ile Gly Arg Cys Leu Leu Val Ala Pro Pro Thr Thr Asp Gly	
	1985	1990 1995 2000
40	Glu Leu Leu Asp Gly Leu Thr Thr Val Leu Ser Glu Arg Gly Ala Ser	
	2005	2010 2015
	Val Ala Arg Leu Glu Val Pro Ile Gly Ala Arg Arg Ala Glu Val Ala	
	2020	2025 2030
45	Glu Leu Leu Lys Pro Ser Met Glu Ser Ala Gly Glu Glu Asn Thr Thr	
	2035	2040 2045
	Val Val Ser Leu Leu Gly Leu Val Pro Ser Thr Asp Ala Val Arg Thr	
50	2050	2055 2060
	Ser Ile Ala Leu Leu Gln Ala Val Ser Asp Ile Gly Val Pro Ala Ala	
	2065	2070 2075 2080
55	Arg Val Trp Ala Leu Thr Arg Arg Ala Val Ala Val Val Pro Gly Glu	
	2085	2090 2095

EP 0 791 655 A2

Thr Pro Gln Asp Ala Gly Ala Gln Leu Trp Gly Phe Gly Arg Val Ala
 2100 2105 2110
 5 Ala Leu Glu Leu Pro Asp Ile Trp Gly Gly Leu Ile Asp Leu Pro Glu
 2115 2120 2125
 Thr Ala Glu Leu Thr Arg Thr Pro Glu Thr Ser Gln Pro Pro Gln Thr
 2130 2135 2140
 10 Pro Glu Arg Leu Pro Gln Thr Pro Asn Arg Arg Ala Leu Glu Leu Ala
 2145 2150 2155 2160
 Ala Ala Val Leu Ala Gly Arg Asp Gly Glu Asp Gln Val Ala Val Arg
 2165 2170 2175
 15 Ala Ser Gly Ile Tyr Gly Arg Arg Val Ser Arg Ala Ala Ala Ala Gly
 2180 2185 2190
 Ala Ala Ser Trp Gln Pro Ser Gly Thr Val Leu Ile Thr Gly Gly Met
 2195 2200 2205
 20 Gly Ala Ile Gly Arg Arg Leu Ala Arg Arg Leu Ala Ala Glu Gly Ala
 2210 2215 2220
 Glu Arg Leu Val Leu Thr Ser Arg Arg Gly Pro Glu Ala Pro Gly Ala
 2225 2230 2235 2240
 25 Ala Glu Leu Ala Glu Glu Leu Arg Gly His Gly Cys Glu Val Val His
 2245 2250 2255
 Ala Ala Cys Asp Val Ala Glu Arg Asp Ala Leu Ala Ala Leu Val Thr
 2260 2265 2270
 30 Ala Tyr Pro Pro Asn Ala Val Phe His Thr Ala Gly Ile Leu Asp Asp
 2275 2280 2285
 Ala Val Ile Asp Thr Leu Ser Pro Glu Ser Phe Glu Thr Val Arg Gly
 2290 2295 2300
 35 Ala Lys Val Cys Gly Ala Glu Leu Leu His Gln Leu Thr Ala Asp Ile
 2305 2310 2315 2320
 Lys Gly Leu Asp Ala Phe Val Leu Phe Ser Ser Val Thr Gly Thr Trp
 2325 2330 2335
 Gly Asn Ala Gly Gln Gly Ala Tyr Ala Ala Ala Asn Ala Ala Leu Asp
 2340 2345 2350
 40 Ala Leu Ala Glu Arg Arg Arg Ala Ala Gly Leu Pro Ala Thr Ser Val
 2355 2360 2365
 Ala Trp Gly Leu Trp Gly Gly Gly Gly Met Ala Ala Gly Ala Gly Glu
 2370 2375 2380
 50 Glu Ser Leu Ser Arg Arg Gly Leu Arg Ala Met Asp Pro Asp Ala Ala
 2385 2390 2395 2400
 Val Asp Ala Leu Leu Gly Ala Met Gly Arg Asn Asp Val Cys Val Thr
 2405 2410 2415
 55

EP 0 791 655 A2

Val Val Asp Val Asp Trp Glu Arg Phe Ala Pro Ala Thr Asn Ala Ile
2420 2425 2430

5 Arg Pro Gly Arg Leu Phe Asp Thr Val Pro Glu Ala Arg Glu Ala Leu
2435 2440 2445

Thr Ala Ala Gly Thr Thr Ser Ala Thr Pro Asp Gly Ala Pro Glu Leu
2450 2455 2460

10 Ala Arg Arg Leu Ser Met Leu Asn Glu Thr Glu Arg Leu Arg Lys Leu
2465 2470 2475 2480

Val Glu Leu Val Arg Thr Glu Ala Ala Phe Val Leu Arg His Pro Asn
2485 2490 2495

15 Thr Asp Ala Ile Gly Ala Glu Arg Pro Phe Lys Ser Ala Gly Phe Asp
2500 2505 2510

Ser Leu Thr Ser Leu Glu Leu Arg Asn Arg Leu Asn Ala Gly Thr Gly
2515 2520 2525

20 Leu Lys Leu Pro Ala Thr Val Ile Phe Asp His Pro Ser Pro Thr Ala
2530 2535 2540

Leu Ala Arg Leu Leu Leu Asp Arg Leu Thr Gly Ala Gly Ala Pro Ala
2545 2550 2555 2560

25 Pro Ala Ala Asp Glu Pro Pro Leu Pro Val Ala Val Ala Asp Asp Asp
2565 2570 2575

Pro Val Val Ile Val Gly Met Ala Cys Arg Phe Pro Gly Gly Ala Gly
2580 2585 2590

30 Thr Pro Glu Ala Leu Trp Lys Leu Val Thr Glu Glu Arg Asp Val Ile
2595 2600 2605

Gly Ala Ala Pro Thr Asp Arg Gly Trp Asp Leu Asp Ser Val Tyr Asp
2610 2615 2620

35 Pro Glu Pro Gly Val Ala Gly Lys Thr Tyr Val Arg Glu Gly Gly Phe
2625 2630 2635 2640

40 Leu His Asp Ala Ala Glu Phe Asp Ala Glu Phe Phe Gly Ile Ser Pro
2645 2650 2655

Arg Glu Ala Val Ala Met Asp Pro Gln Gln Arg Leu Leu Leu Glu Thr
2660 2665 2670

45 Ser Trp Glu Ala Ile Glu Arg Ala Gly Ile Asp Pro His Ser Leu His
2675 2680 2685

Gly Ser Arg Thr Gly Val Tyr Val Gly Leu Thr His Gln Glu Tyr Ala
2690 2695 2700

50 Ser Arg Leu His Glu Ala Pro Glu Glu Tyr Glu Gly Tyr Leu Leu Thr
2705 2710 2715 2720

Gly Lys Ser Ala Ser Val Val Ser Gly Arg Ile Ser Tyr Thr Leu Gly
2725 2730 2735

55

EP 0 791 655 A2

Leu Glu Gly Pro Ser Leu Ser Ile Asp Thr Ala Cys Ser Ser Ser Leu
 2740 2745 2750
 Val Ala Leu His Asn Ala Ala Gln Ala Leu Arg Gly Gly Glu Cys Asp
 5 2755 2760 2765
 Met Ala Leu Ala Gly Gly Val Thr Val Met Ala Ala Pro Gly Leu Phe
 2770 2775 2780
 Val Glu Phe Ser Arg Gln Arg Gly Leu Ala Ala Asp Gly Arg Cys Lys
 10 2785 2790 2795 2800
 Ala Phe Ala Asp Gly Ala Asp Gly Thr Ala Trp Ala Glu Gly Ala Gly
 2805 2810 2815
 Val Val Leu Val Glu Arg Leu Ser Asp Ala Arg Arg Leu Gly His Pro
 15 2820 2825 2830
 Val Leu Ala Val Val Cys Gly Ser Ala Val Asn Gln Asp Gly Ala Ser
 2835 2840 2845
 Asn Gly Leu Thr Ala Pro Ser Gly Pro Ser Gln Glu Arg Val Ile Arg
 20 2850 2855 2860
 Gln Ala Leu Ala Asn Ala Arg Leu Thr Val Ala Asp Val Asp Val Val
 25 2865 2870 2875 2880
 Glu Ala His Gly Thr Gly Thr Arg Leu Gly Asp Pro Ile Glu Ala Gln
 2885 2890 2895
 Ala Leu Leu Gly Thr Tyr Gly Arg Asp Arg Asp Ala Glu Cys Pro Val
 30 2900 2905 2910
 Trp Leu Gly Ser Leu Lys Ser Asn Ile Gly His Ala Gln Ala Ala Ala
 2915 2920 2925
 Gly Val Ala Gly Val Ile Lys Met Val Leu Ala Met Arg Tyr Gly Trp
 35 2930 2935 2940
 Leu Pro Arg Thr Leu His Val Asp Glu Pro Ser Arg His Val Asp Trp
 2945 2950 2955 2960
 Ser Ala Gly Gly Val Arg Leu Leu Thr Glu Ala Arg Glu Trp Pro Gly
 40 2965 2970 2975
 Val Asp Arg Pro Arg Arg Ala Ala Val Ser Ala Phe Gly Val Ser Gly
 2980 2985 2990
 Thr Asn Ala His Leu Ile Leu Glu Ala Pro Glu Ala Leu Glu Ala Leu
 45 2995 3000 3005
 Glu Ala Thr Asp Ala Pro Glu Ala Pro Glu Ala Pro Glu Ala Pro Asp
 50 3010 3015 3020
 Val Thr Asp Val Thr Glu Ala Leu Glu Ala Pro Asp Ala Thr Glu Ala
 3025 3030 3035 3040
 Glu Gly Ala Lys Ala Pro Gly Ser Pro Glu Glu Ala Gln Pro Ala Val
 55 3045 3050 3055

EP 0 791 655 A2

Gly Val Val Pro Val Val Val Ser Gly Arg Ser Arg Val Val Val Arg
3060 3065 3070

5 Glu Ala Ala Gly Arg Leu Ala Glu Val Val Glu Ala Gly Gly Val Gly
3075 3080 3085

Leu Ala Asp Val Ala Val Thr Met Ala Gly Arg Ser Arg Phe Gly Tyr
3090 3095 3100

10 Arg Ala Val Val Leu Ala Arg Gly Glu Ala Glu Leu Ala Gly Arg Leu
3105 3110 3115 3120

Arg Ala Leu Ala Gly Gly Asp Pro Asp Ala Gly Val Val Thr Gly Ala
3125 3130 3135

15 Val Val Asp Pro Glu Thr Gly Ser Gly Gly Gly Gly Val Val Leu Val
3140 3145 3150

Phe Pro Gly Gln Gly Thr Gln Trp Val Gly Met Gly Ala Gly Leu Leu
3155 3160 3165

20 Gly Ser Ser Glu Val Phe Ala Ala Ser Met Arg Glu Cys Ala Arg Ala
3170 3175 3180

Leu Ser Val His Val Glu Trp Asp Leu Leu Glu Val Val Ser Gly Gly
3185 3190 3195 3200

25 Ala Gly Leu Glu Arg Val Asp Val Val Gln Pro Val Thr Trp Ala Val
3205 3210 3215

Met Val Ser Leu Ala Arg Tyr Trp Gln Ala Met Gly Val Asp Val Ala
3220 3225 3230

30 Ala Val Val Gly His Ser Gln Gly Glu Ile Ala Ala Ala Thr Val Ala
3235 3240 3245

Gly Ala Leu Ser Leu Glu Asp Ala Ala Ala Val Val Ala Leu Arg Ala
3250 3255 3260

35 Gly Leu Ile Gly Arg Tyr Leu Ala Gly Arg Gly Ala Met Ala Ala Val
3265 3270 3275 3280

40 Pro Leu Pro Ala Gly Glu Val Glu Ala Gly Leu Ala Lys Trp Pro Gly
3285 3290 3295

Val Gln Val Ala Ala Val Asn Gly Pro Ala Ser Thr Val Val Ser Gly
3300 3305 3310

45 Asp Arg Arg Ala Val Ala Gly Tyr Val Ala Val Cys Gln Ala Glu Gly
3315 3320 3325

Val Gln Ala Arg Leu Ile Pro Val Asp Tyr Ala Ser His Ser Arg His
3330 3335 3340

50 Val Glu Asp Leu Lys Gly Glu Leu Glu Arg Val Leu Ser Gly Ile Arg
3345 3350 3355 3360

55 Pro Arg Ser Pro Arg Val Pro Val Cys Ser Thr Val Ala Gly Glu Gln
3365 3370 3375

EP 0 791 655 A2

Pro Gly Glu Pro Val Phe Asp Ala Gly Tyr Trp Phe Arg Asn Leu Arg
3380 3385 3390

5 Asn Arg Val Glu Phe Ser Ala Val Val Gly Gly Leu Leu Glu Gln Gly
3395 3400 3405

His Arg Arg Phe Ile Glu Val Ser Ala His Pro Val Leu Val His Ala
3410 3415 3420

10 Ile Glu Gln Thr Ala Glu Ala Ala Asp Arg Ser Val His Ala Thr Gly
3425 3430 3435 3440

Thr Leu Arg Arg Gln Asp Asp Ser Pro His Arg Leu Leu Thr Ser Thr
3445 3450 3455

15 Ala Glu Ala Trp Ala His Gly Ala Thr Leu Thr Trp Asp Pro Ala Leu
3460 3465 3470

Pro Pro Gly His Leu Thr Thr Leu Pro Thr Tyr Pro Phe Asn His His
3475 3480 3485

20 His Tyr Trp Ala Val Thr Ser Pro Ala Gly Val Gly Asp Ala Ala Ala
3490 3495 3500

Gly Arg Phe Gly Met Thr Trp Glu Asp His Pro Phe Leu Arg Gly Gly
3505 3510 3515 3520

25 Leu Pro Leu Ala Asp Ser Gly Glu Arg Val Phe Ala Gly Arg Leu Ala
3525 3530 3535

Gly Ser Glu His Asp Trp Leu Thr Asp His Ala Val Ser Gly Val Thr
3540 3545 3550

30 Leu Leu Pro Gly Thr Ala Phe Val Glu Phe Ala Leu His Ala Gly Ala
3555 3560 3565

35 Ala Thr Gly Cys Gly Arg Leu Glu Glu Leu Ser Val Glu Ala Pro Leu
3570 3575 3580

Val Leu Pro Ala Ala Gly Gly Val Arg Val Gln Met Arg Val Ser Ala
3585 3590 3595 3600

40 Ala Asp Glu Ser Gly Arg Arg Arg Val Ala Ile His Ser Ala Pro Glu
3605 3610 3615

Ala Ala Val His Ser Ala Ala Glu Gly Gly Asp Ser Ala Gly Val Trp
3620 3625 3630

45 Thr Arg His Gly Glu Gly Thr Leu Val Pro Asp Pro Glu Pro Thr Pro
3635 3640 3645

Pro Asp Ala Asp Trp Ala Arg Ala Trp Pro Pro Ala Gly Glu Arg Val
3650 3655 3660

50 Glu Pro Ala Glu Leu Tyr Glu Arg Phe Gly Ala Leu Gly Tyr Glu Tyr
3665 3670 3675 3680

Gly Glu Ala Phe Ala Gly Val Arg Ala Val Trp Arg Gln Pro Asp Ala
3685 3690 3695

55

EP 0 791 655 A2

Leu Leu Ala Glu Val Leu Leu Pro Asp Arg Ala Ser Thr Gly Ala Gly
3700 3705 3710

5 Arg Phe Gly Val His Pro Ala Leu Leu Asp Ala Ala Leu Gln Pro Trp
3715 3720 3725

Ile Ala Gly Gly Leu Leu Glu Val Pro Glu Asp Ala Val Leu Leu Pro
3730 3735 3740

10 Phe Ala Trp Gln Gly Val Ser Leu Tyr Ala Thr Gly Ala Gly Ala Leu
3745 3750 3755 3760

Arg Val Arg Leu Thr Lys Ala Gly Asp Gly Ala Val Ser Leu Gln Ala
3765 3770 3775

15 Ala Asp Thr Ser Gly Ala Ala Val Leu Ser Leu Gly Ala Leu Val Met
3780 3785 3790

Arg Pro Leu Ala Arg Arg Lys Leu Asp Val Leu Leu Gly Thr Asp Ala
3795 3800 3805

20 Gly Glu Arg Ser Leu Tyr Arg Val Glu Trp Gln Pro Arg Leu Leu Pro
3810 3815 3820

Ala Gly Pro Pro Arg Ser Trp Ala Val Leu Gly Pro Asp Ala Asp Arg
3825 3830 3835 3840

25 Leu Ala Gly Thr Pro Gly Leu Gly Asp Gln Pro Asp Gly Gly Pro Thr
3845 3850 3855

Ala Leu Tyr Pro Glu Val Arg Ala Leu Arg Lys Ala Leu Ala Ala Gly
3860 3865 3870

30 Ala Pro Arg Pro Glu Ala Val Val Leu Pro Val Leu Ser Gly Ala Gly
3875 3880 3885

Ala Thr Pro Glu Ser Val Arg Gln Thr Thr Glu Arg Cys Leu Thr Ala
3890 3895 3900

35 Leu Gln Asp Trp Leu Asp Ala Glu Glu Leu Val Asp Thr Pro Leu Ile
3905 3910 3915 3920

40 Val Leu Thr Arg Gly Ala Val Ala Ala Val Pro Gly Glu Glu Ile Gly
3925 3930 3935

Asp Leu Ala Cys Ala Gly Val Trp Gly Leu Val Arg Ser Ala Arg Ser
3940 3945 3950

45 Glu His Pro Gly Arg Phe Ala Leu Val Asp Thr Asp Gly His Pro Asp
3955 3960 3965

Asp Arg Thr Ala Leu Pro Leu Ala Leu Arg Ala Val Leu Asp Gly Ala
3970 3975 3980

50 Gly Gln Leu Ser Leu Arg Ala Gly Thr Ala Arg Thr Pro Val Leu Leu
3985 3990 3995 4000

Arg Ala Gly Thr Pro Glu Glu Gln Arg Gly Pro Ala Phe Asp Pro Ala
4005 4010 4015

55

EP 0 791 655 A2

Gly Thr Val Leu Val Thr Gly Ala Thr Gly Thr Leu Gly Arg Leu Leu
 4020 4025 4030
 5 Ala Arg His Leu Ala Ala Glu His Gly Val Arg His Leu Leu Leu
 4035 4040 4045
 Ser Arg Gly Gly Arg Ala Ala Glu Gly Ala Asp Glu Leu Ala Ala Glu
 4050 4055 4060
 10 Leu Ala Gly Leu Glu Ala Glu Pro Cys Phe Ala Ala Cys Asp Ala Ala
 4065 4070 4075 4080
 Asp Arg Glu Ala Leu Ala Arg Val Leu Ala Glu Val Pro Ala Asp Arg
 4085 4090 4095
 15 Pro Leu Thr Gly Val Ile His Ala Ala Gly Val Leu Asp Asp Gly Thr
 4100 4105 4110
 Leu Asp Ala Leu Thr Pro Glu Arg Ile Gly Thr Val Met Arg Pro Lys
 4115 4120 4125
 20 Ala Asp Ala Ala Leu Asn Leu His Glu Leu Thr Arg Thr Ser Pro Leu
 4130 4135 4140
 Ser Val Phe Ala Val Phe Ser Gly Ala Ala Gly Ile Leu Gly Arg Pro
 4145 4150 4155 4160
 25 Gly Gln Ala Asn Tyr Ala Ala Ala Asn Thr Phe Leu Asp Ala Leu Ala
 4165 4170 4175
 Gln His Arg Arg Ala His Gly Leu Pro Ala Val Ser Leu Ala Trp Gly
 4180 4185 4190
 30 Leu Trp Gly Gly Ala Thr Gly Met Thr Gly His Leu Ser Gly Thr Asp
 4195 4200 4205
 Leu Arg Arg Met Arg Arg Ser Gly Ile Ala Pro Met Thr His Asp Gln
 4210 4215 4220
 35 Gly Leu Ala Leu Phe Asp Arg Ala Leu Ala Ala Ser Ala Glu Asp Pro
 4225 4230 4235 4240
 40 Leu Leu Val Pro Met Arg Leu Asp Leu Ala Ala Leu Val Arg Glu Arg
 4245 4250 4255
 Ala Glu His Gly Pro Asp Ala Val Pro Gly Pro Leu Leu Gly Leu Leu
 4260 4265 4270
 45 Pro Ala Arg Ala Ala Val Arg Gln Ala Ala Ala Pro Val Arg Gly Gly
 4275 4280 4285
 Ala Pro Ala Pro Ala Gly Gly Glu Gly Thr Ala Glu Arg Leu Ala Gly
 4290 4295 4300
 50 Leu Gly Glu Glu Ala Arg Leu Arg Glu Leu Val Arg Leu Val Arg Ala
 4305 4310 4315 4320
 Glu Val Ser Gly Val Leu Gly Tyr Ser Gly Pro Asp Ala Val Glu Pro
 4325 4330 4335
 55

EP 0 791 655 A2

Gly Arg Pro Phe Lys Asp Leu Gly Phe Asp Ser Leu Thr Ala Val Glu
 4340 4345 4350
 5 Leu Arg Asn Arg Leu Gly Ala Ala Thr Gly Leu Arg Leu Pro Thr Ala
 4355 4360 4365
 Leu Val Phe Asp Arg Pro Thr Ser Gln Ala Val Ala Glu Tyr Leu Ala
 4370 4375 4380
 10 Ala Glu Leu Ala Gly Pro Arg Asp Gly Gly Asp Thr Ala Ala Ala Ala
 4385 4390 4395 4400
 Phe Glu Gly Leu Glu Ala Leu Ala Ala Val Gly Ala Leu Ala Glu
 4405 4410 4415
 15 Asp Asp Leu Arg Arg Asp Val Leu Arg Arg Arg Leu Thr Glu Leu Ala
 4420 4425 4430
 Ala Ala Leu Thr Pro Gln Gly Arg Asn Pro Ser Ala Pro Ala Pro Ala
 4435 4440 4445
 20 Pro Ser Asp Leu Asp Glu Arg Leu Asp Ser Ala Asn Asp Asp Asp Leu
 4450 4455 4460
 Phe Ala Phe Ile Glu Glu Gln Leu *
 4465 4470
 25

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 1865 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Thr Ala Glu Leu Val Ala Thr Arg Lys Arg Leu Gly Ala Leu Glu
 1 5 10 15
 40 Glu Arg Ala Arg Glu Pro Ile Ala Val Val Ala Met Ser Cys Arg Tyr
 20 25 30
 Pro Gly Gly Val Thr Thr Pro Glu Asp Leu Trp Arg Leu Leu Ala Asp
 35 40 45
 45 Glu Arg Asp Ala Val Ser Gly Leu Pro Arg Asp Arg Gly Trp Asp Leu
 50 55 60
 Asp Ala Leu Tyr Asp Pro Asp Gly Gly Pro Gly Thr Ser Tyr Ala Arg
 65 70 75 80
 50 Glu Gly Gly Phe Leu Ser His Cys Ala Gly Phe Asp Ala Glu Phe Phe
 85 90 95
 Gly Ile Ser Pro Arg Glu Ala Leu Ala Met Asp Pro Gln Gln Arg Leu
 100 105 110
 55

EP 0 791 655 A2

	Leu	Leu	Glu	Thr	Ser	Trp	Glu	Ala	Leu	Glu	Arg	Ala	Gly	Val	Thr	Ala	
			115					120					125				
5	Asp	Arg	Ala	Arg	Gly	Ser	Arg	Thr	Gly	Val	Tyr	Ala	Gly	Val	Met	Tyr	
			130				135					140					
	Asp	Asp	Tyr	Gly	Ala	Arg	Val	Leu	Tyr	Gly	Ala	Gly	Ala	Gly	Pro	Pro	
			145			150					155				160		
10	Glu	Asp	Leu	Glu	Gly	Tyr	Leu	Val	Asn	Gly	Ser	Ala	Gly	Ser	Ile	Ala	
				165						170					175		
	Ser	Gly	Arg	Val	Ser	Tyr	Thr	Phe	Gly	Leu	Arg	Gly	Pro	Ala	Val	Thr	
				180					185					190			
15	Val	Asn	Thr	Ala	Cys	Ser	Ser	Ser	Leu	Val	Ser	Leu	His	Leu	Ala	Val	
			195					200					205				
	Arg	Ala	Leu	Arg	Asn	Gly	Glu	Cys	Asp	Met	Ala	Leu	Ala	Gly	Gly	Ala	
			210				215					220					
20	Thr	Val	Leu	Ser	Thr	Pro	Thr	Val	Leu	Val	Asp	Phe	Ser	Arg	Gln	Arg	
						230					235				240		
	Gly	Leu	Ala	Pro	Asp	Gly	Arg	Cys	Lys	Ala	Phe	Ala	Asp	Ser	Ala	Asp	
25					245					250				255			
	Gly	Thr	Ser	Trp	Ala	Glu	Gly	Ala	Gly	Met	Leu	Leu	Leu	Gln	Arg	Leu	
				260					265					270			
30	Ser	Asp	Ala	Arg	Arg	Glu	Gly	Arg	Pro	Val	Leu	Ala	Val	Ile	Arg	Gly	
			275					280					285				
	Ser	Ala	Val	Asn	Gln	Asp	Gly	Ala	Ser	Asn	Gly	Leu	Thr	Ala	Pro	Asn	
			290				295					300					
35	Gly	Arg	Ala	Gln	Arg	Gln	Val	Ile	Glu	Asp	Ala	Leu	Arg	Asp	Ala	Gly	
					310					315					320		
	Val	Gly	Pro	Asp	Gln	Val	Asp	Ala	Val	Glu	Ala	His	Gly	Thr	Gly	Thr	
					325					330					335		
40	Glu	Leu	Gly	Asp	Pro	Ile	Glu	Ala	Gly	Ala	Leu	Leu	Ala	Thr	Tyr	Gly	
				340					345					350			
	Thr	Ala	Arg	Thr	Ala	Glu	Arg	Pro	Leu	Trp	Leu	Gly	Ser	Leu	Lys	Ser	
				355				360					365				
45	Asn	Ile	Gly	His	Thr	Gln	Ala	Ala	Ala	Gly	Val	Ala	Gly	Val	Ile	Lys	
			370				375					380					
	Met	Val	Leu	Ala	Met	Arg	His	Gly	Arg	Leu	Pro	Arg	Thr	Leu	His	Val	
50			385			390					395				400		
	Asp	Arg	Pro	Thr	Thr	Arg	Val	Asp	Trp	Glu	Lys	Gly	Gly	Val	Arg	Leu	
					405					410					415		
55	Leu	Thr	Glu	Pro	Val	Pro	Trp	Pro	Gly	Glu	Ala	Gly	Glu	Pro	Arg	Arg	
				420					425					430			

EP 0 791 655 A2

	Ala Gly Val Ser Ser Phe Gly Ala Ser Gly Thr Asn Ala His Val Val	
	435 440 445	
5	Leu Glu Ser Val Pro Ala Gly Glu Pro Pro Ala Ala Gly Arg Pro Glu	
	450 455 460	
	Asp Thr Gly Gly Ala Trp Thr Val Ser Gly Arg Gly Pro Ala Ala Leu	
	465 470 475 480	
10	Arg Ala Gln Ala Ala Arg Leu Tyr Asp Ala Leu Thr Gly Thr Gly Thr	
	485 490 495	
	Gly Thr Gly Gln Gly Ala Gly Gln Gly Ala Gly Pro Gly Thr Ala Glu	
	500 505 510	
15	Val Ala Gly Ala Leu Ala His Ala Arg Thr Ala Phe Arg His Arg Ala	
	515 520 525	
	Val Val Leu Gly Gly Asn Arg Ala Glu Leu Leu Ala Gly Leu Arg Glu	
	530 535 540	
20	Leu Ala Glu Glu Glu His Pro Gly Pro Arg Val Val Thr Gly Thr Ala	
	545 550 555 560	
	Pro Ala Thr Glu Arg Arg Thr Ala Phe Leu Phe Ser Gly Gln Gly Ser	
	565 570 575	
25	Gln Arg Ala Gly Ser Gly Arg Gly Leu Tyr Arg Arg His Pro Val Phe	
	580 585 590	
	Ala Arg Ala Leu Asp Glu Val Cys Ala Ala Leu Glu Pro His Leu His	
	595 600 605	
30	Arg Pro Leu Arg Asp Leu Met Phe Ala Glu Pro Gly Ser Pro Glu Ala	
	610 615 620	
	Glu Pro Leu Asp Arg Thr Glu Phe Thr Gln Pro Ala Leu Phe Ala Leu	
	625 630 635 640	
	Gln Thr Ala Leu Phe Arg Leu Ala Glu His His Gly Leu Arg Ala Glu	
	645 650 655	
40	Ala Leu Cys Gly His Ser Val Gly Glu Ile Ala Ala Ala His Ala Ala	
	660 665 670	
	Gly Val Leu Thr Leu Pro Asp Ala Ala Arg Leu Val Ala Ala Arg Gly	
	675 680 685	
45	Arg Leu Met Gln Ala Leu Pro Ala Gly Gly Ala Met Ala Ala Leu Arg	
	690 695 700	
	Ala Thr Ala Glu Glu Ile Ala Pro Leu Leu Glu Arg Arg Ala Gly Glu	
	705 710 715 720	
50	Leu Ala Leu Ala Ala Val Asn Gly Pro Ser Ser Val Val Val Ser Gly	
	725 730 735	
	Asp Glu Ala Ala Val Leu Glu Leu Leu Glu Gln Trp Arg Ala Glu Gly	
	740 745 750	
55		

EP 0 791 655 A2

	Arg	Glu	Ala	Arg	Arg	Leu	Ala	Val	Ser	His	Ala	Phe	His	Ser	Pro	Arg	
			755					760					765				
5	Met	Asp	Gly	Met	Leu	Thr	Gln	Phe	Asp	Arg	Val	Ala	Arg	Thr	Leu	Thr	
		770					775					780					
	Phe	Ala	Pro	Pro	Thr	Ile	Pro	Leu	Val	Ser	Thr	Leu	Thr	Gly	Thr	Pro	
	785					790					795					800	
10	Val	Thr	Glu	Glu	Thr	Leu	Cys	Thr	Ala	Asp	His	Trp	Val	Arg	Gln	Ala	
					805					810					815		
	Arg	Glu	Pro	Val	Arg	Phe	Leu	Asp	Ala	Met	Arg	Thr	Leu	Arg	Ala	Asp	
				820					825					830			
15	Gly	Ile	Asp	Thr	Phe	Val	Glu	Leu	Gly	Pro	Asp	Gly	Val	Leu	Ser	Ala	
		835						840					845				
	Met	Ala	Arg	Asp	Cys	Ala	Asp	Asp	Arg	Pro	Asp	Gly	Asp	Thr	Thr	Gly	
	850						855					860					
20	Ala	Gly	Asp	Gly	Glu	Thr	Pro	Asp	Pro	Leu	Leu	Thr	Leu	Pro	Leu	Leu	
	865					870					875					880	
	Arg	Arg	Ser	Val	Pro	Glu	Thr	Gly	Asp	Ala	Glu	His	Pro	Gly	Gly	Phe	
					885					890					895		
25	Glu	Arg	Ala	Leu	Ala	Thr	Ala	Tyr	Ala	His	Gly	Val	Pro	Leu	Arg	Leu	
				900				905						910			
	Ala	Pro	Ala	Pro	Asp	Ala	Ala	Ser	Leu	Ala	Val	Ala	Ala	Glu	Leu	Pro	
30			915					920					925				
	Thr	Tyr	Ala	Phe	Gln	Arg	Thr	His	Tyr	Trp	Leu	Asp	Ala	Pro	Ala	Ala	
	930					935						940					
35	Pro	Ala	Ala	Leu	Pro	Ala	Gly	Leu	Asp	Asp	Ala	Gly	His	Pro	Leu	Leu	
	945				950					955					960		
	Ser	Ala	Ala	Leu	Asp	Leu	Pro	Gly	Gly	Arg	Gly	Thr	Val	Trp	Thr	Gly	
				965						970					975		
40	Ala	Leu	Ser	Ala	Ala	Thr	Leu	Pro	Trp	Ala	Ala	Asp	His	Ser	Val	His	
				980					985					990			
	Gly	Arg	Thr	Val	Leu	Pro	Gly	Thr	Ala	Leu	Leu	Asp	Leu	Ala	Leu	His	
		995						1000					1005				
45	Ala	Ala	Pro	Arg	Val	Gly	Glu	Leu	Thr	Phe	Glu	Ala	Pro	Leu	Val	Leu	
	1010						1015					1020					
	Pro	Glu	Asp	Gly	Glu	Val	Arg	Leu	Arg	Val	Val	Leu	Ala	Glu	Pro	Asp	
50	1025					1030					1035				1040		
	Ala	Ser	Gly	Val	Arg	Glu	Leu	Ser	Val	His	Ser	Ala	Gly	Glu	Asp	Gly	
				1045						1050					1055		
55	Gly	Trp	Thr	Arg	His	Ala	Thr	Ala	Val	Leu	Asp	Thr	Gly	Thr	Thr	Thr	
				1060					1065					1070			

EP 0 791 655 A2

	Ala Gly Glu Pro Ala Gly Ala Pro Pro Ala Ala Trp Pro Pro Gly Asp	
	1075	1080 1085
5	Ala Glu Pro Leu Asp Leu Ala Ala Glu Tyr Glu Arg Phe Ala Asp Ala	
	1090	1095 1100
	Gly Ile Gly Tyr Gly Pro Ala Phe Arg Gly Leu Arg Ser Ala Trp Arg	
	1105	1110 1115 1120
10	Asp Gly Asp Ala Ile Leu Ala Asp Val Arg Leu Pro Gly Glu Leu Ala	
	1125	1130 1135
	Gly Glu Ala Asp Arg Tyr Gly Ile His Pro Ala Leu Leu Asp Ala Ala	
	1140	1145 1150
15	Leu His Thr Ala Ala Ala Ala Leu Gly Gly Ala His Gly Met Leu Pro	
	1155	1160 1165
	Phe Thr Trp Asn Gly Val Thr Leu His Ala Arg Gly Ala His Ala Ile	
	1170	1175 1180
20	Arg Val Arg Leu Thr Pro Ala Gly Pro Asp Ala Val Ala Val Thr Ala	
	1185	1190 1195 1200
	Val Asp Pro Ala Gly Arg Pro Val Phe Thr Ala Ala Ser Leu Thr Leu	
25	1205	1210 1215
	Arg Pro Val Thr Thr Gly Gln Leu Thr Ala Ala Glu Ala Ala Arg Ala	
	1220	1225 1230
	Pro Leu Tyr Arg Val Arg Trp Thr Gly Leu Pro Asp Thr Gly Thr Ala	
30	1235	1240 1245
	Arg Asp His Thr Trp Ala Val Ala Gly Gly Pro Gly Asp Leu Leu Pro	
	1250	1255 1260
35	Gly Glu Thr Pro His His Pro Asp Leu Ala Ser Ala Leu Ala Asp Thr	
	1265	1270 1275 1280
	Gly Thr Ala Pro Phe Arg Val Leu Ala Asp Leu Arg Gly Tyr Gly Thr	
	1285	1290 1295
40	Ala Thr Pro Arg Glu Leu Ala Ser Gln Ala Leu Ala Leu Val Gln Gln	
	1300	1305 1310
	Trp Ala Asp Ala Ala Glu Ala Ala Glu Gly Arg Leu Val Leu Val Thr	
	1315	1320 1325
45	Arg Arg Ala Val Asp Ile Gly Asp Gly Val Thr Asp Pro Ala Ala Ala	
	1330	1335 1340
	Thr Val Trp Gly Leu Val Arg Ala Ala Gln Ser Glu His Pro Gly Cys	
50	1345	1350 1355 1360
	Phe Ala Leu Leu Asp Thr Asp Asp Ser Pro Arg Ser Arg Gln Leu Leu	
	1365	1370 1375
55	Pro Arg Val Ala Gly Thr Ala Glu Gln Leu Ala Leu Arg Asp Gly Thr	
	1380	1385 1390

EP 0 791 655 A2

	Leu Leu Ala Pro Ser Leu Thr Arg Ala Thr Leu Pro Ala Gly Ala Arg	
	1395	1400 1405
5	Leu Pro Ala Leu Asp Gly Thr Val Leu Ile Thr Gly Gly Thr Gly Ser	
	1410	1415 1420
	Leu Gly Ala Glu Ala Ala Arg His Leu Val Thr Arg His Gly Ala Arg	
	1425	1430 1435 1440
10	Arg Leu Leu Leu Thr Ser Arg Ser Gly Pro Gln Ala Pro Gly Ala Ala	
		1445 1450 1455
	Glu Leu Val Ala Glu Leu Ala Ala Leu Gly Ala His Ala Asp Val Ala	
		1460 1465 1470
15	Ala Cys Asp Val Ala Asp Arg Ala Ala Leu Arg Ala Leu Leu Asp Arg	
		1475 1480 1485
	Val Pro Ala Gly His Pro Leu Thr Ala Val Leu His Thr Ala Gly Val	
		1490 1495 1500
20	Leu Asp Asp Gly Val Leu Thr Ala Gln Thr Pro Gln Arg Leu Ala Ala	
		1505 1510 1515 1520
	Val Leu Arg Pro Lys Ala Asp Ala Val Arg Asn Leu His Glu Leu Thr	
		1525 1530 1535
25	Gln Gly His Ala Leu Ser Ala Phe Ile Leu Tyr Ser Ser Ala Ala Gly	
		1540 1545 1550
	Val Leu Gly Ser Ala Gly Gln Ser Gly Tyr Ala Ala Ala Asn Ala Tyr	
		1555 1560 1565
30	Leu Asp Ser Phe Ala Val Trp Arg Arg Ser Arg Gly Leu Pro Ala Val	
		1570 1575 1580
	Ser Leu Gly Trp Gly Pro Trp Asp Gly Gly Gly Met Ala Ser Gly Leu	
		1585 1590 1595 1600
	Gly Gly Thr Asp Thr Ala Arg Leu Arg Arg Ser Gly Ile Ala Pro Leu	
		1605 1610 1615
40	Ser Arg Ala Glu Gly Leu Ala Ala Leu Asp Ala Ala Leu Ala Ala Gly	
		1620 1625 1630
	Gly Asp Asp Thr Ala Pro Ala His Leu Leu Pro Ile Arg Val Asp Ala	
		1635 1640 1645
45	Val Thr Leu Arg Gly Ala Asp Thr Val Pro Ala Val Leu Arg Asp Leu	
		1650 1655 1660
	Ala Gly Thr Ala Pro Ser Ala Ala Glu Arg Pro Pro Gly Thr Pro Glu	
		1665 1670 1675 1680
50	Asp Thr Asn Ala Pro Leu Ala Asp Val Thr Gln Leu His Gly Arg Glu	
		1685 1690 1695
	Arg Lys Glu Ala Leu Thr Gly Phe Val Arg Ala Gln Val Ala Ala Val	
		1700 1705 1710
55		

EP 0 791 655 A2

Leu Gly His Pro Thr Ser Asp Thr Ile Asp Val Arg Arg Ser Phe Lys
1715 1720 1725

5 Glu Ala Gly Phe Asp Ser Leu Thr Ala Val Glu Leu Arg Asn Arg Leu
1730 1735 1740

Arg Ala Ala Thr Gly Leu Lys Leu Pro Ala Thr Leu Val Phe Asp His
1745 1750 1755 1760

10 Pro Thr Pro Leu Ala Leu Ala Gly Phe Leu His Arg Glu Leu Pro Gly
1765 1770 1775

Ala Glu Ala Ser Leu Met Ser Ala Ile Asp Thr Leu Arg His Arg Leu
1780 1785 1790

15 Arg Asp Ala Leu Ala Asp Asp Ala Ala Asp Asp Ala Leu Arg Asp Gln
1795 1800 1805

Ile Thr Arg Arg Leu Glu Thr Leu Leu Ala Gly Ile Ala Arg Thr Glu
1810 1815 1820

20 Glu Pro Ala Pro Ala Thr Ala Ala Ala Asp Asp Gly Ser Gly Ala Gly
1825 1830 1835 1840

Asp Val Ala Glu Arg Leu Ser Thr Ala Ser Asp Asp Glu Leu Phe Glu
1845 1850 1855

25 Leu Leu Asp Ser Gly Phe Thr Pro *

1860 1865

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3730 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ser Thr Glu Asn Ser Thr Asn Val Pro Ala Ser Glu Asp Lys Leu
1 5 10 15

Arg Ala Tyr Leu Arg Arg Ala Met Ala Asp Leu His Glu Ser Arg Glu
20 25 30

Arg Leu Arg Ala Thr Glu Ala Arg Ala Gln Glu Pro Ile Ala Val Val
35 40 45

Gly Met Gly Cys Arg Phe Pro Gly Gly Val Gly Ser Pro Glu Ala Leu
50 55 60

Trp Arg Leu Val Val Glu Gly Val Asp Ala Val Ser Pro Phe Pro Gly
65 70 75 80

55 Asp Arg Gly Trp Asp Val Glu Gly Leu Tyr Asp Pro Glu Pro Gly Val
85 90 95

EP 0 791 655 A2

Ala Gly Lys Ser Tyr Val Arg Glu Gly Gly Phe Leu His Asp Ala Ala
100 105 110

5 Glu Phe Asp Ala Glu Phe Phe Gly Ile Ser Pro Arg Glu Ala Val Ala
115 120 125

Met Asp Pro Gln Gln Arg Leu Leu Leu Glu Thr Ser Trp Glu Ala Ile
130 135 140

10 Glu Arg Ala Gly Ile Asp Pro His Ser Leu His Gly Ser Arg Thr Gly
145 150 155 160

Val Tyr Ala Gly Val Met Tyr His Asp Tyr Gly Thr Gly Gln Thr Ser
165 170 175

15 Ala Thr Asp Thr Ser Gly Tyr Ser Gly Thr Gly Thr Ser Gly Ser Val
180 185 190

Val Ser Gly Arg Val Ala Tyr Thr Leu Gly Leu Glu Gly Pro Ala Val
195 200 205

20 Thr Val Asp Thr Ala Cys Ser Ser Ser Leu Val Ala Leu His Leu Ala
210 215 220

25 Val Gln Ala Leu Arg Gly Gly Glu Cys Asp Met Ala Leu Ala Gly Gly
225 230 235 240

Val Thr Val Met Ala Gly Pro Gly Met Phe Val Glu Phe Ser Arg Gln
245 250 255

30 Arg Gly Leu Ala Ala Asp Gly Arg Cys Lys Ala Phe Ala Asp Gly Ala
260 265 270

Asp Gly Thr Ala Trp Ala Glu Gly Ala Gly Val Val Leu Val Glu Arg
275 280 285

35 Leu Ser Asp Ala Arg Arg Leu Gly His Pro Val Leu Ala Val Val Cys
290 295 300

Gly Ser Ala Val Asn Gln Asp Gly Ala Ser Asn Gly Leu Thr Ala Pro
305 310 315 320

40 Ser Gly Pro Ser Gln Glu Arg Val Ile Arg Gln Ala Leu Ala Asn Ala
325 330 335

Arg Leu Thr Val Ala Asp Val Asp Val Val Glu Ala His Gly Thr Gly
340 345 350

45 Thr Arg Leu Gly Asp Pro Ile Glu Ala Gln Ala Leu Leu Gly Thr Tyr
355 360 365

Gly Arg Asp Arg Asp Gly Gly Arg Pro Val Trp Leu Gly Ser Leu Lys
370 375 380

50 Ser Asn Ile Gly His Ala Gln Ala Ala Ala Gly Val Ala Gly Val Ile
385 390 395 400

55 Lys Met Val Leu Ala Met Arg Tyr Gly Trp Leu Pro Arg Thr Leu His
405 410 415

EP 0 791 655 A2

Val Asp Glu Pro Ser Arg His Val Asp Trp Ser Ala Gly Gly Val Trp
420 425 430

5 Leu Leu Thr Glu Ala Arg Glu Trp Pro Gly Val Asp Arg Pro Arg Arg
435 440 445

Ala Ala Val Ser Ala Phe Gly Val Ser Gly Thr Asn Ala His Leu Ile
450 455 460

10 Leu Glu Ala Pro Asp Thr Ala Glu Ala Glu Ser Ala Thr Thr Pro Val
465 470 475 480

Arg Ser Glu Val Ser Glu Ser Ala Ala Val Phe Asp Ala Arg Ser Gly
485 490 495

15 Val Val Pro Val Val Val Ser Gly Arg Ser Arg Val Val Val Arg Glu
500 505 510

Ala Ala Gly Arg Leu Ala Glu Val Val Glu Ala Gly Gly Val Gly Leu
515 520 525

20 Ala Asp Val Ala Val Thr Met Ala Gly Arg Ser Arg Phe Gly Tyr Arg
530 535 540

Ala Val Val Leu Ala Arg Gly Glu Ala Glu Leu Ala Gly Arg Leu Arg
545 550 555 560

Ala Leu Ala Gly Gly Asp Pro Asp Ala Gly Val Val Thr Gly Ala Val
565 570 575

30 Val Asp Pro Glu Thr Gly Ser Gly Gly Gly Gly Val Val Leu Val Phe
580 585 590

Pro Gly Gln Gly Thr Gln Trp Val Gly Met Gly Ala Gly Leu Leu Gly
595 600 605

35 Ser Ser Glu Val Phe Ala Ala Ser Met Arg Glu Cys Ala Arg Ala Leu
610 615 620

Ser Val His Val Gly Trp Asp Leu Leu Glu Val Val Ser Gly Gly Ala
625 630 635 640

40 Gly Leu Glu Arg Val Asp Val Val Gln Pro Val Thr Trp Ala Val Met
645 650 655

Val Ser Leu Ala Arg Tyr Trp Gln Ala Met Gly Val Asp Val Ala Ala
660 665 670

45 Val Val Gly His Ser Gln Gly Glu Ile Ala Ala Ala Thr Val Ala Gly
675 680 685

Ala Leu Ser Leu Glu Asp Ala Ala Ala Val Val Ala Leu Arg Ala Gly
690 695 700

50 Leu Ile Gly Arg Tyr Leu Ala Gly Arg Gly Ala Met Ala Ala Val Pro
705 710 715 720

55 Leu Pro Ala Gly Glu Val Glu Ala Gly Leu Ala Lys Trp Pro Gly Val
725 730 735

EP 0 791 655 A2

Glu Val Ala Ala Val Asn Gly Pro Ala Ser Thr Val Val Ser Gly Asp
 740 745 750
 5 Arg Arg Ala Val Ala Gly Tyr Val Ala Val Cys Gln Ala Glu Gly Val
 755 760 765
 Gln Ala Arg Leu Ile Pro Val Asp Tyr Ala Ser His Ser Arg His Val
 770 775 780
 10 Glu Asp Leu Lys Gly Glu Leu Glu Arg Val Leu Ser Gly Ile Arg Pro
 785 790 795 800
 Arg Ser Pro Arg Val Pro Val Cys Ser Thr Val Ala Gly Glu Gln Pro
 805 810 815
 15 Gly Glu Pro Val Phe Asp Ala Gly Tyr Trp Phe Arg Asn Leu Arg Asn
 820 825 830
 Arg Val Glu Phe Ser Ala Val Val Gly Gly Leu Leu Glu Glu Gly His
 835 840 845
 20 Arg Arg Phe Ile Glu Val Ser Ala His Pro Val Leu Val His Ala Ile
 850 855 860
 Glu Gln Thr Ala Glu Ala Ala Asp Arg Ser Val His Ala Thr Gly Thr
 865 870 875 880
 25 Leu Arg Arg Gln Asp Asp Ser Pro His Arg Leu Leu Thr Ser Thr Ala
 885 890 895
 Glu Ala Trp Ala His Gly Ala Thr Leu Thr Trp Asp Pro Ala Leu Pro
 900 905 910
 Pro Gly His Leu Thr Thr Leu Pro Thr Tyr Pro Phe Asn His His His
 915 920 925
 30 Tyr Trp Leu Asp Thr Thr Pro Thr Thr Pro Ala Thr Thr Thr Gln Ser
 930 935 940
 Pro Thr Asp Ala Gln Asn Pro Ala Asp Ala Leu Pro Tyr Lys Val Ser
 945 950 955 960
 40 Trp Lys Arg Leu Arg Asp Gln Asp Ser Leu Thr Ala Arg Leu Asp Gly
 965 970 975
 Arg Trp Leu Leu Val Val Pro Glu Ala Ser Ala Asp Pro Ser Val Ala
 980 985 990
 45 Glu Gly Val Ala Arg Glu Leu Thr Ala Arg Gly Ala Thr Val Glu Ser
 995 1000 1005
 Leu Thr Val Glu Pro Gly Ala Asp Arg Ser Arg Leu Arg Gly Leu Leu
 1010 1015 1020
 50 Val Asp Ala Thr Glu Arg Asp Glu Ala Gly Pro Leu Arg Gly Ile Val
 1025 1030 1035 1040
 Ser Leu Leu Ala Leu Ala Gly Asp His Ala Gly Ala Asp Gly Ala Arg
 1045 1050 1055

Pro Val Val Pro Ala Gly Leu Ala Ala Ser Leu Ala Leu Ile Gln Ala
 1060 1065 1070
 5 Ala Gly Asp Ala Gly Thr Glu Ala Gly Leu Trp Ala Val Thr Arg Gly
 1075 1080 1085
 Ala Val Ala Ala Val Pro Gly Asp Val Pro Ala Pro Ser Gln Ala Leu
 1090 1095 1100
 10 Leu Trp Gly Phe Gly Arg Val Ala Gly Ile Glu Leu Pro His Cys Trp
 1105 1110 1115 1120
 Gly Gly Leu Leu Asp Leu Pro Thr Gly Pro Gly Asp Ser Gly Phe Arg
 1125 1130 1135
 15 Gln Leu Ala Ala Thr Leu Ala Gly Arg Pro Ala Glu Asp Gln Val Ala
 1140 1145 1150
 Leu Arg Ala Ser Gly Ala Tyr Gly Arg Arg Leu Val Arg Ala Ser Ala
 1155 1160 1165
 20 Ala Gly Gly Ala Asp Gly Trp Arg Pro Arg Gly Thr Val Leu Val Val
 1170 1175 1180
 Gly Asp Thr Ala Glu Val Ala Gly Pro Leu Val Arg Trp Leu Leu Gly
 1185 1190 1195 1200
 25 Asn Gly Ala Arg Arg Val Thr Leu Ser Gly Leu Ser Gly Pro Leu Pro
 1205 1210 1215
 Glu Glu Leu Ala Asp Val Ala Ala Arg Val Thr Val Ala Pro Cys Asp
 1220 1225 1230
 30 Pro Ala Asp Arg Pro Ala Leu Arg Thr Leu Leu Ala Glu Gln Ala Pro
 1235 1240 1245
 35 Thr Ala Val Leu Val Ala Pro Pro Ala Val Pro Pro Thr Pro Leu Ala
 1250 1255 1260
 Glu Met Thr Ala Glu Ala Leu Ala Ile Ala Leu Ser Ala Lys Thr Gly
 1265 1270 1275 1280
 40 Leu Val Asp Arg Leu Asp Ser Leu Leu Asp Glu Pro Asp Pro Leu Leu
 1285 1290 1295
 Glu Asp Gly Glu Leu Asp Ala Phe Val Val Phe Ser Ser Val Ala Gly
 1300 1305 1310
 45 Val Trp Gly Gly Ala Gly Gln Gly Gly Tyr Ala Ala Gly Thr Ala Tyr
 1315 1320 1325
 Leu Asp Ala Leu Ala Glu Cys Arg Arg Ala Gly Gly Leu Pro Val Thr
 1330 1335 1340
 50 Ser Val Ala Trp Thr Pro Trp Leu Gly Thr Pro Ala Ala Asp Ser Leu
 1345 1350 1355 1360
 55 Gly Glu Gln Met Ser Arg Ala Gly Ile Thr Pro Leu Asp Pro Ala Ala
 1365 1370 1375

EP 0 791 655 A2

Ser Leu Asp Ala Leu Ala Arg Ala Val Gly Arg Arg Ala Gly Cys Val
1380 1385 1390

5 Thr Val Ala Asp Ile Asp Trp Glu Arg Phe Ala Ser Ala Tyr Thr Ala
1395 1400 1405

Thr Arg Pro Thr Pro Met Phe Asp Glu Val Pro Glu Val Arg Arg Ile
1410 1415 1420

10 Gln Ala Ala Trp Ala Glu Ala Glu Ala Asp Ala Ala Arg Ser Gly Ala
1425 1430 1435 1440

Gly Gly Asp Ser Gln Leu Leu Arg Ser Leu Arg Gly Arg Pro Glu Glu
1445 1450 1455

15 Ala Gln Leu Ala Glu Leu Leu Arg Leu Val Arg Thr His Ala Ala Ala
1460 1465 1470

Val Leu Gly Leu Gly Ser Pro Gly Ala Val Glu Ala Arg Arg Ser Phe
1475 1480 1485

20 Lys Asp Leu Gly Phe Asn Ser Val Thr Ala Val Glu Leu Arg Asn Arg
1490 1495 1500

Leu Lys Glu Ala Thr Gly Leu Arg Leu Glu Val Ser Leu Val Phe Asp
1505 1510 1515 1520

25 His Pro Asp Pro Ala Ser Leu Ala Arg His Leu Leu Asp Leu Ala Leu
1525 1530 1535

Gly Gln Glu Pro Glu Glu Thr Pro Arg Ala Phe Ala Leu Glu Pro Ala
1540 1545 1550

Pro Asn Gly Glu Pro Ile Ala Ile Val Ser Met Ala Cys Arg Met Pro
1555 1560 1565

35 Gly Gly Val Ser Thr Pro Glu Glu Leu Trp Arg Leu Leu Arg Asp Gly
1570 1575 1580

Lys Asp Ala Ile Gly Pro Phe Pro Ala Asn Arg Gly Trp Asp Leu Glu
1585 1590 1595 1600

40 Asn Leu Tyr Asp Pro Asp Pro Asp Ala Asp Gly Arg Thr Tyr Val Arg
1605 1610 1615

Glu Gly Gly Phe Leu His Glu Ala Pro Asp Phe Asp Pro Ser Phe Phe
1620 1625 1630

45 Gly Ile Ser Pro Arg Glu Ala Leu Ala Met Asp Pro Gln Gln Arg Leu
1635 1640 1645

Leu Leu Glu Thr Ser Trp Glu Ala Leu Glu Arg Ala Gly Ile Asp Pro
1650 1655 1660

50 Ala Arg Leu Arg Gly Ser Arg Thr Gly Val Phe Val Gly Thr Asn Gly
1665 1670 1675 1680

Gln His Tyr Met Pro Leu Leu Gln Asn Gly Gly Asp Ser Phe Asp Gly
1685 1690 1695

55

Tyr Leu Gly Thr Gly Asn Ser Ala Ser Val Met Ser Gly Arg Leu Ser
 1700 1705 1710
 5 Tyr Val Phe Gly Leu Glu Gly Pro Ala Val Thr Val Asp Thr Ala Cys
 1715 1720 1725
 Ser Ala Ser Leu Val Ala Leu His Leu Ala Val Gln Ala Met Arg Arg
 1730 1735 1740
 10 Gly Glu Cys Asp Met Ala Leu Val Gly Gly Ala Thr Val Met Ser Thr
 1745 1750 1755 1760
 Pro Glu Met Leu Val Glu Phe Ser Arg Gln Arg Val Ile Ser Ala Asn
 1765 1770 1775
 15 Gly Arg Ser Arg Ala Phe Ala Ala Gly Ala Asp Gly Val Ala Leu Gly
 1780 1785 1790
 Glu Gly Val Gly Val Leu Leu Val Glu Arg Leu Ser Asp Ala Glu Arg
 1795 1800 1805
 20 Asn Gly His Pro Val Leu Ala Val Val Arg Gly Ser Ala Val Asn Gln
 1810 1815 1820
 Asp Gly Ala Ser Asn Gly Leu Thr Ala Pro Asn Gly Pro Ser Gln Gln
 1825 1830 1835 1840
 25 Arg Val Ile Arg Gln Ala Leu Ala Asp Ala Gly Leu Arg Pro Glu Asp
 1845 1850 1855
 30 Ile Asp Ala Val Glu Ala His Gly Thr Gly Thr Glu Leu Gly Asp Pro
 1860 1865 1870
 Ile Glu Ala Glu Ala Leu Leu Ala Thr Tyr Gly Arg Thr Arg Thr Ala
 1875 1880 1885
 35 Asp Arg Pro Leu Trp Leu Gly Ser Leu Lys Ser Asn Ile Gly His Thr
 1890 1895 1900
 Gln Ala Ala Ala Gly Val Ala Gly Val Ile Lys Met Val Leu Ala Leu
 1905 1910 1915 1920
 40 Gly Asn Glu Thr Leu Pro Arg Thr Leu His Val Asp Glu Pro Thr Pro
 1925 1930 1935
 Arg Val Asp Trp Ser Ser Gly Ala Val Ser Leu Leu Thr Glu Pro Val
 1940 1945 1950
 45 Asp Trp Pro Ala Gly Pro Ser Ala Pro Arg Arg Ala Ala Val Ser Ser
 1955 1960 1965
 Phe Gly Ile Ser Gly Thr Asn Ala His Thr Ile Leu Glu Gln Ala Pro
 1970 1975 1980
 50 Val Pro Ala Glu Ser Arg Pro Gly Thr Glu Pro Ala Asp Gly Thr Gly
 1985 1990 1995 2000
 55 Ala Trp Glu Asn Val Thr Val Pro Leu Leu Leu Ser Gly His Thr Glu
 2005 2010 2015

EP 0 791 655 A2

Ala Ala Leu Arg Glu Gln Ser Thr Arg Leu Leu Asn Asp Leu Leu Glu
2020 2025 2030

5 His Pro Asp Glu His Pro Ala Asp Val Gly Tyr Thr Leu Ile Thr Gly
2035 2040 2045

Arg Ala His Phe Gly His Arg Ala Ala Val Ile Gly Glu Ser Arg Glu
2050 2055 2060

10 Glu Leu Leu Asp Ala Leu Lys Ala Leu Ala Glu Gly Arg Glu His His
2065 2070 2075 2080

Thr Val Val Arg Gly Asp Gly Thr Ala His Pro Asp Arg Arg Val Val
2085 2090 2095

15 Phe Val Phe Pro Gly Gln Gly Ser Gln Trp Pro Ser Met Ala Arg Asp
2100 2105 2110

Leu Leu Asp Arg Ala Pro Ala Phe Arg Glu Thr Ala Lys Ala Cys Asp
2115 2120 2125

20 Ala Ala Leu Ser Val His Leu Asp Trp Ser Val Leu Asp Val Leu Gln
2130 2135 2140

Glu Lys Pro Asp Ala Pro Pro Leu Ser Arg Val Asp Val Val Gln Pro
2145 2150 2155 2160

25 Val Leu Phe Thr Met Met Leu Ser Leu Ala Ala Cys Trp Arg Asp Leu
2165 2170 2175

30 Gly Val His Pro Ala Ala Val Val Gly His Ser Gln Gly Glu Ile Ala
2180 2185 2190

Ala Ala Cys Val Ala Gly Ala Leu Ser Leu Glu Asp Ala Ala Arg Ile
2195 2200 2205

35 Val Ala Leu Arg Ser Arg Ala Trp Leu Thr Leu Ala Gly Lys Gly Gly
2210 2215 2220

Met Ala Ala Val Ser Leu Pro Glu Ala Arg Leu Arg Glu Arg Ile Glu
2225 2230 2235 2240

40 Arg Phe Gly Gln Arg Leu Ser Val Ala Ala Val Asn Ser Pro Gly Thr
2245 2250 2255

Ala Ala Val Ala Gly Asp Val Asp Ala Leu Arg Glu Leu Leu Ala Glu
2260 2265 2270

45 Leu Thr Ala Glu Gly Ile Arg Ala Lys Pro Ile Pro Gly Val Asp Thr
2275 2280 2285

Ala Gly His Ser Ala Gln Val Asp Gly Leu Lys Glu His Leu Phe Glu
2290 2295 2300

50 Val Leu Ala Pro Val Ser Pro Arg Ser Ser Asp Ile Pro Phe Tyr Ser
2305 2310 2315 2320

55 Thr Val Thr Gly Ala Pro Leu Asp Thr Glu Arg Leu Asp Ala Gly Tyr
2325 2330 2335

Trp Tyr Arg Asn Met Arg Glu Pro Val Glu Phe Glu Lys Ala Val Arg
 2340 2345 2350
 5 Ala Leu Ile Ala Asp Gly Tyr Asp Leu Phe Leu Glu Cys Asn Pro His
 2355 2360 2365
 Pro Met Leu Ala Met Ser Leu Asp Glu Thr Leu Thr Asp Ser Gly Gly
 2370 2375 2380
 10 His Gly Thr Val Met His Thr Leu Arg Arg Gln Lys Gly Ser Ala Lys
 2385 2390 2395 2400
 Asp Phe Gly Met Ala Leu Cys Leu Ala Tyr Val Asn Gly Leu Glu Ile
 2405 2410 2415
 15 Asp Gly Glu Ala Leu Phe Gly Pro Asp Ser Arg Arg Val Asn Pro Pro
 2420 2425 2430
 Thr Tyr Pro Phe Gln Arg Glu Arg Tyr Trp Tyr His Pro Thr Ser Gly
 2435 2440 2445
 20 Arg Arg Gly Asp Ile Thr Ala Ala Gly Val Ala Glu Ala Glu His Pro
 2450 2455 2460
 Leu Leu Gly Ala Gly Val Glu Leu Pro Glu Thr Gly Gly Thr Val Tyr
 2465 2470 2475 2480
 25 Thr Ala Arg Phe Gly Pro Asp Ser Arg Pro Trp Leu Ala Asp His Ala
 2485 2490 2495
 30 Leu Leu Gly Thr Val Leu Leu Pro Gly Thr Ala Ile Leu Asp Leu Val
 2500 2505 2510
 Leu Trp Ala Gly Glu Arg Ser Gly Cys Gly Arg Val Gly Glu Leu Ala
 2515 2520 2525
 35 Leu Gln Ala Pro Leu Val Leu Pro Asp Ser Gly Asp Val Glu Leu Arg
 2530 2535 2540
 Leu Leu Val Gly Gly Pro Asp Glu Glu Lys Arg Arg Thr Val Thr Val
 2545 2550 2555 2560
 40 His Ala Arg Pro Ala Ala Ala Gly Ala Glu Ala Pro Trp Thr Arg His
 2565 2570 2575
 Ala Glu Ala Val Val Leu Pro Ala Thr Gly Glu Glu Pro Thr Pro Ala
 2580 2585 2590
 45 Pro Arg Pro Val Pro Glu Pro Ala Gly Thr Thr Asp Pro Ala Ala Phe
 2595 2600 2605
 Tyr Ala Glu Phe Ala Glu Arg Gly Tyr Asp Tyr Gly Pro Ala Phe Gln
 2610 2615 2620
 50 Gly Phe Thr Ala Gly Ala Arg His Gly Glu Asp Val Val Ala Glu Val
 2625 2630 2635 2640
 55 Ala Leu Pro Ser Gly Leu Val Ala Asp Ala Arg His His Arg Leu His
 2645 2650 2655

EP 0 791 655 A2

Pro Ala Leu Leu Asp Ala Ala Leu Gln Ala Met Ile Leu Gly Thr Phe
2660 2665 2670

5 Phe Ala Asp Asp Gly Arg Ala Arg Met Pro Phe Ala Val Arg Gly Val
2675 2680 2685

Arg Leu His Thr Ala Gly Ala Asp Arg Leu Arg Val Leu Ile Ser Pro
2690 2695 2700

10 Ala Gly Asp Glu Thr Val Arg Leu Leu Cys Thr Asp Leu Ala Thr Gly
2705 2710 2715 2720

Ala Pro Val Leu Glu Ile Asp Glu Leu Val Val Arg Pro Val Ser Gly
2725 2730 2735

15 Glu Gln Leu Ala Ala Gly Ala Pro Gly Arg Asn Gly Gly Glu Leu Tyr
2740 2745 2750

Arg Val Asp Trp Thr Val Leu Pro Glu Pro Ala Glu Val Pro Ala Pro
2755 2760 2765

20 Arg Trp Ala Leu Leu Gly Glu Asp His Ala Gly Leu Ala Asp Val Leu
2770 2775 2780

Gly Gly Thr Gly Gly Gly Cys Glu Arg Tyr Asp Thr Leu Thr Gly Leu
2785 2790 2795 2800

Leu Glu Ala Thr Thr Arg Ser Ala Gly Gly Ile Leu Pro Asp Ile Val
2805 2810 2815

30 Ala Leu Ser Leu Pro Thr Ala Pro Glu Pro Gly Pro Gln Ala Val Arg
2820 2825 2830

Glu Val Leu Ser Gln Ala Leu Asp Ala Ala Gln Ala Trp Leu Ala Ala
2835 2840 2845

35 Gly Ala Glu Thr Ala Ser Ala Arg Leu Val Phe Val Thr Gly Gly Ala
2850 2855 2860

Val Ala Thr Thr Ala Asp Glu Thr Val Arg Asp Ile Ala Ala Ala Ala
2865 2870 2875 2880

40 Val Trp Gly Leu Val Arg Ser Ala Gln Ser Glu Glu Pro Asp Arg Met
2885 2890 2895

Val Leu Leu Asp Leu Asp Gly Glu Arg Pro Thr Ala Arg Thr Leu Ala
2900 2905 2910

45 Ala Ala Leu Ala Ser Gly Glu Pro Gln Leu Ala Val Arg Gly Ser Thr
2915 2920 2925

Val Ala Ala Pro Arg Leu Ala Pro Ala Gly Pro Gly Pro Glu Asp Leu
2930 2935 2940

50 Val Pro Pro Ala Gly Thr Thr Ala Trp Arg Leu Thr Pro Gly Gly Gly
2945 2950 2955 2960

Thr Leu Glu Glu Leu Ser Leu Ala Pro Ala Pro Asp Ala Glu Glu Pro
2965 2970 2975

55

Leu Ala Pro Gly Gln Val Arg Ile Ala Val Arg Ala Ala Gly Val Asn
 2980 2985 2990
 5 Phe Arg Asp Ala Leu Ile Ala Leu Gly Met Tyr Pro Gly Lys Gly Thr
 2995 3000 3005
 Met Gly Ala Glu Gly Ala Gly Val Val Val Glu Thr Ala Pro Asp Val
 3010 3015 3020
 10 Thr Gly Leu Ser Ala Gly Asp Arg Val Leu Gly Met Trp Asn Gly Gly
 3025 3030 3035 3040
 Phe Gly Pro Leu Val Val Ala Asp His Arg Met Val Ala Pro Ile Pro
 3045 3050 3055
 15 His Gly Trp Ser Tyr Ala Glu Ala Ala Ser Val Pro Ala Val Leu Leu
 3060 3065 3070
 Thr Ser Tyr Tyr Ala Leu Thr Arg Leu Ala Arg Ala Arg Thr Gly Gln
 3075 3080 3085
 20 Thr Val Leu Val His Ala Ala Ala Gly Gly Val Gly Met Ala Thr Leu
 3090 3095 3100
 Gln Leu Ala Arg His Leu Gly Leu Glu Val Tyr Ala Thr Ala Ser Thr
 3105 3110 3115 3120
 25 Gly Lys Trp Asp Ala Leu Gln Lys His Gly Ile Pro Asp Asp Arg Ile
 3125 3130 3135
 Ala Asp Ser Arg Thr Leu Asp Phe Ala Glu Arg Phe Leu Ser Arg Thr
 3140 3145 3150
 30 Gly Gly Arg Gly Val Asp Ile Val Leu Asn Ser Leu Ala Gly Glu Phe
 3155 3160 3165
 Val Asp Ala Ser Leu Arg Leu Leu Pro Arg Gly Gly His Phe Leu Glu
 3170 3175 3180
 35 Leu Gly Lys Ala Asp Val Arg Asp Pro Arg Arg Ile Ala Ala Ala His
 3185 3190 3195 3200
 40 Pro Gly Thr Asp Tyr Arg Ala Phe Asp Leu Val Gln Ala Gly Pro Asp
 3205 3210 3215
 Thr Val Gly Glu Met Leu Gly Glu Leu Leu Glu Leu Phe Ala Ala Gly
 3220 3225 3230
 45 Ala Leu Arg Pro Leu Pro Leu Thr Ala Tyr Gly Ile Arg Asp Ala Arg
 3235 3240 3245
 Thr Ala Leu Arg Thr Leu Ser Gln Ala Arg His Thr Gly Lys Leu Val
 3250 3255 3260
 50 Leu Thr Val Pro Ala Gly Phe Asp Thr His Arg Thr Val Leu Leu Thr
 3265 3270 3275 3280
 Gly Gly Thr Gly Thr Leu Gly Gln Thr Leu Ala Arg His Leu Val Asn
 3285 3290 3295
 55

EP 0 791 655 A2

Arg His Gly Val Arg His Leu Leu Leu Ala Gly Arg Thr Gly Ala Ala
3300 3305 3310

5 Ala Glu Gly Val Ala Glu Leu Ile Gly Glu Leu Gly Glu Leu Gly Ala
3315 3320 3325

Glu Val Arg Val Ala Ala Cys Asp Ala Ala Asp Arg Gln Arg Leu Thr
3330 3335 3340

10 Glu Leu Leu Ala Gly Ile Pro Val Glu His Pro Leu Gly Ala Val Val
3345 3350 3355 3360

His Ala Ala Gly Thr Leu Asp Asp Gly Thr Ile Pro Ser Leu Thr Gly
3365 3370 3375

15 Glu Asn Ile Asp Asn Val Leu Arg Pro Lys Ala Asp Ala Val Leu Asn
3380 3385 3390

Leu His Glu Leu Thr Arg Asp Ala Asp Leu Ser Ala Phe Val Leu Tyr
3395 3400 3405

20 Ser Ser Ser Ser Ala Leu Leu Gly Ser Pro Gly Gln Gly Ala Tyr Ala
3410 3415 3420

Ala Ala Asn Ala Phe Leu Asp Gly Phe Ala Arg Tyr Arg Lys Gly Leu
3425 3430 3435 3440

Gly Leu Pro Ala Leu Ser Leu Ala Trp Gly Leu Trp Gly Ser Asn Ser
3445 3450 3455

30 Arg Met Ala Gly His Leu Asp Gln Ser Gly Met Gln Arg Arg Leu Asn
3460 3465 3470

Arg Ser Gly Ile Met Ala Leu Thr Asp Ala Glu Gly Leu Ala Leu Phe
3475 3480 3485

35 Asp Ala Ala Gln Asp Gly Gly Asp Ala Leu Leu Val Pro Met Arg Leu
3490 3495 3500

Asn Arg Thr Ala Leu Arg Ala Ser Gly Arg Ile Thr Pro Phe Leu Ser
3505 3510 3515 3520

40 Gly Leu Ala Gly Gly Gly Pro Ala Ala Gly Glu Arg Arg Pro Glu Val
3525 3530 3535

Ala Ala Val Ser Gly Thr Leu Ala Glu Arg Leu Thr Gly Leu Thr Ala
3540 3545 3550

45 Gln Glu Gly His Ala Leu Val Leu Ala Glu Ile Arg Ala His Ala Ala
3555 3560 3565

Ala Val Leu Gly His Gly Ser Asp Asp Ser Ile Pro Glu Asp Arg Ala
3570 3575 3580

50 Phe Lys Asp Leu Gly Phe Asp Ser Leu Thr Ala Val Glu Met Arg Asn
3585 3590 3595 3600

Arg Leu Ser Ala Ala Thr Gly Leu Arg Leu Pro Ala Thr Leu Val Phe
3605 3610 3615

55

Asp His Pro Thr Pro Gly Glu Leu Ala Gly His Leu Ser Ala Glu Leu
 3620 3625 3630
 5 Ser Ala Asp Asp Ala Pro Gly Ser Ala Ser Pro Leu Thr Glu Leu Asp
 3635 3640 3645
 Arg Phe Glu Ala Leu Phe Thr Ala Leu Ala Pro Gly Thr Thr Lys Asp
 3650 3655 3660
 10 Thr Pro Gly Gly Ala Gly Ala Leu Met Ile Asp Glu Ala Glu Arg Gln
 3665 3670 3675 3680
 Glu Ile Ala Gly Arg Leu Ala Ala Leu Ala Gly Leu Trp Asn Arg Leu
 3685 3690 3695
 15 His Gly Thr Thr Thr Ala Pro Glu Asp Gly Asp Thr Val Ala Asp Ala
 3700 3705 3710
 Leu Glu Ala Ala Asp Asp His Glu Ile Phe Ala Phe Leu Asp Glu Arg
 3715 3720 3725
 20 Phe *
 3730

25 (2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1612 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

35 Met Ala Asn Ala Asn Glu Gln Gln Leu Arg Ala Tyr Leu Lys Arg Ala
 1 5 10 15
 Thr Thr Glu Leu His Arg Thr Ser Glu Gln Leu Arg Glu Glu Arg Ala
 20 25 30
 40 Arg Ala His Glu Pro Ile Ala Val Val Gly Met Ala Cys Arg Tyr Pro
 35 40 45
 Gly Gly Ala Asn Thr Pro Glu Gln Phe Trp Glu Leu Leu Asp Thr Gly
 50 55 60
 45 Thr Asp Ala Ala Ala Pro Met Pro Ser Asp Arg Gly Trp Asp Thr His
 65 70 75 80
 50 Gly Leu Tyr Asp Pro Asp Pro Ala Ala Ala Gly Arg Thr Tyr Cys Arg
 85 90 95
 Glu Gly Gly Phe Leu His Asp Ala Gly Asp Phe Asp Ala Asp Phe Phe
 100 105 110
 55 Gly Ile Ser Pro Arg Glu Ala Val Ala Met Asp Pro Gln Gln Arg Leu
 115 120 125

Leu Leu Glu Thr Ser Trp Glu Ala Ile Glu Ala Ala Gly Ile Asp Pro
 130 135 140
 5 Arg Gly Leu Arg Gly Ser Arg Thr Gly Val Tyr Val Gly Ala Trp Asp
 145 150 155 160
 Ser Gly Tyr Thr Gly Gln Ala His Ala Pro Ser Ala Glu Leu Glu Ala
 165 170 175
 10 Asp Leu Leu Thr Gly Gly Val Val Ser Phe Thr Ser Gly Arg Ile Ala
 180 185 190
 Tyr Thr Leu Gly Leu Glu Gly Pro Ala Leu Thr Val Asp Thr Ala Cys
 195 200 205
 15 Ser Ser Ser Leu Val Ala Leu His Asn Ala Ala Gln Ala Leu Arg Arg
 210 215 220
 Gly Glu Cys Asp Leu Ala Leu Ala Gly Gly Val Thr Val Met Ala Thr
 225 230 235 240
 20 Pro Ala Val Phe Val Gln Phe Ala Arg Gln Arg Gly Leu Ala Pro Asp
 245 250 255
 Gly Arg Cys Lys Ala Phe Ala Asp Ala Ala Asp Gly Phe Gly Pro Ala
 260 265 270
 25 Glu Gly Val Gly Met Val Leu Val Glu Arg Leu Ser Asp Ala Arg Arg
 275 280 285
 Leu Gly His Pro Val Leu Ala Val Val Cys Gly Ser Ala Val Asn Gln
 290 295 300
 Asp Gly Ala Ser Asn Gly Leu Thr Ala Pro Ser Gly Pro Ser Gln Glu
 305 310 315 320
 35 Arg Val Ile Arg Gln Ala Leu Gly Asn Ala Arg Leu Thr Val Ala Asp
 325 330 335
 Val Asp Val Val Glu Ala His Gly Thr Gly Thr Arg Leu Gly Asp Pro
 340 345 350
 40 Ile Glu Ala Gln Ala Leu Leu Gly Thr Tyr Gly Arg Asp Arg Asp Gly
 355 360 365
 Gly Arg Pro Val Trp Leu Gly Ser Leu Lys Ser Asn Ile Gly His Ala
 370 375 380
 45 Gln Ala Ala Ala Gly Val Ala Gly Val Ile Lys Met Val Leu Ala Met
 385 390 395 400
 Arg Tyr Gly Trp Leu Pro Arg Thr Leu His Val Asp Glu Pro Ser Arg
 405 410 415
 50 His Val Asp Trp Ser Ala Gly Gly Val Arg Leu Leu Thr Glu Ala Arg
 420 425 430
 Glu Trp Pro Gly Val Asp Arg Pro Arg Arg Ala Ala Val Ser Ala Phe
 435 440 445
 55

EP 0 791 655 A2

Gly Val Ser Gly Thr Asn Ala His Leu Ile Leu Glu Ala Pro Asp Thr
 450 455 460
 5 Ala Glu Ala Glu Ser Ala Thr Thr Pro Val Arg Ser Glu Val Ser Glu
 465 470 475 480
 Ser Ala Ala Val Leu Asp Ala Arg Ser Gly Val Val Pro Val Val Val
 485 490 495
 10 Ser Gly Arg Ser Arg Val Val Val Arg Glu Ala Ala Gly Arg Leu Ala
 500 505 510
 Glu Val Val Glu Ala Gly Gly Val Gly Leu Ala Asp Val Ala Val Thr
 515 520 525
 15 Met Ala Gly Arg Ser Arg Phe Gly Tyr Arg Ala Val Val Leu Ala Arg
 530 535 540
 Gly Glu Ala Glu Leu Ala Gly Arg Leu Arg Ala Leu Ala Gly Gly Asp
 545 550 555 560
 20 Pro Asp Ala Gly Val Val Thr Gly Ala Val Val Asp Pro Glu Thr Gly
 565 570 575
 Ser Gly Gly Gly Gly Val Val Leu Val Phe Pro Gly Gln Gly Thr Gln
 580 585 590
 25 Trp Val Gly Met Gly Ala Gly Leu Leu Gly Ser Ser Glu Val Phe Ala
 595 600 605
 Ala Ser Met Arg Glu Cys Ala Arg Ala Leu Ser Val His Val Gly Trp
 610 615 620
 Asp Leu Leu Glu Val Val Ser Gly Gly Ala Gly Leu Glu Arg Val Asp
 625 630 635 640
 35 Val Val Gln Pro Val Thr Trp Ala Val Met Val Ser Leu Ala Arg Tyr
 645 650 655
 Trp Gln Ala Met Gly Val Asp Val Ala Ala Val Val Gly His Ser Gln
 660 665 670
 40 Gly Glu Ile Ala Ala Ala Thr Val Ala Gly Ala Leu Ser Leu Glu Asp
 675 680 685
 Ala Ala Ala Val Val Ala Leu Arg Ala Gly Leu Ile Gly Arg Tyr Leu
 690 695 700
 45 Ala Gly Arg Gly Ala Met Ala Ala Val Pro Leu Pro Ala Gly Glu Val
 705 710 715 720
 Glu Ala Gly Leu Ala Lys Trp Pro Gly Val Glu Val Ala Ala Val Asn
 725 730 735
 50 Gly Pro Ala Ser Thr Val Val Ser Gly Asp Arg Arg Ala Val Ala Gly
 740 745 750
 Tyr Val Ala Val Cys Gln Ala Glu Gly Val Gln Ala Arg Leu Ile Pro
 755 760 765

Val Asp Tyr Ala Ser His Ser Arg His Val Glu Asp Leu Lys Gly Glu
 770 775 780
 5 Leu Glu Arg Val Leu Ser Gly Ile Arg Pro Arg Ser Pro Arg Val Pro
 785 790 795 800
 Val Cys Ser Thr Val Ala Gly Glu Gln Pro Gly Glu Pro Val Phe Asp
 805 810 815
 10 Ala Gly Tyr Trp Phe Arg Asn Leu Arg Asn Arg Val Glu Phe Ser Ala
 820 825 830
 Val Val Gly Gly Leu Leu Glu Glu Gly His Arg Arg Phe Ile Glu Val
 835 840 845
 15 Ser Ala His Pro Val Leu Val His Ala Ile Glu Gln Thr Ala Glu Ala
 850 855 860
 Ala Asp Arg Ser Val His Ala Thr Gly Thr Leu Arg Arg Gln Asp Asp
 865 870 875 880
 20 Ser Pro His Arg Leu Leu Thr Ser Thr Ala Glu Ala Trp Ala His Gly
 885 890 895
 Ala Thr Leu Thr Trp Asp Pro Ala Leu Pro Pro Gly His Leu Thr Thr
 900 905 910
 25 Leu Pro Thr Tyr Pro Phe Asn His His His Tyr Trp Leu Asp Thr Thr
 915 920 925
 Pro Thr Thr Pro Ala Thr Thr Thr Gln Ser Pro Thr Asp Ala Trp Arg
 930 935 940
 Tyr Arg Val Thr Trp Lys Ala Leu Thr Glu Glu Ser Thr Pro Ala Ser
 945 950 955 960
 35 Ser Pro Ser Gly His Trp Leu Leu Val Thr Pro Pro Thr Pro Glu Gly
 965 970 975
 Arg Thr Leu Gly Asp Arg Ala Ala Gly Ala Leu Ala Arg Gln Gly Ala
 980 985 990
 40 Thr Val Glu Arg Leu Val Val Asp Pro Val Ala Val Gly Arg Asp Gly
 995 1000 1005
 Leu Ala Ala Arg Leu Gly Glu Arg Trp Asp Gly Val Leu Ser Leu Leu
 1010 1015 1020
 45 Gly Ala Asp Glu Arg Pro Leu Pro Arg His Pro Ala Leu Asn Arg Ala
 1025 1030 1035 1040
 Val Met Gly Thr Thr Leu Leu Ala Gln Ala Ala Leu Asp Ala Gly Cys
 1045 1050 1055
 50 Glu Ala Arg Ile Trp Ala Val Thr Arg Glu Ala Val Ala Val Ser Pro
 1060 1065 1070
 Ser Glu Val Pro Arg Asp Ala Gly Ala Gln Leu Trp Gly Leu Gly Arg
 1075 1080 1085

Gly Ile Ala Leu Glu His Pro Ser Leu Trp Gly Gly Leu Ile Asp Leu
 1090 1095 1100
 5 Pro Ala Val Pro Asp Glu Arg Ala Trp Ala Arg Ala Val Arg Arg Leu
 1105 1110 1115 1120
 Val Pro His Gly Glu Asp Gln Ile Ala Ala Arg Ala Ser Gly Ala Tyr
 1125 1130 1135
 10 Gly Arg Arg Leu Leu Pro Ala Pro Pro Ala Ala Ser Arg Arg Thr Cys
 1140 1145 1150
 Thr Pro Ser Gly Thr Val Leu Val Thr Gly Gly Thr Gly Ala Leu Gly
 1155 1160 1165
 15 Gly His Leu Ala Arg Arg Leu Ala Arg Gly Gly Thr Gly His Leu Val
 1170 1175 1180
 Leu Thr Ser Arg Arg Gly Pro Asp Ala Pro Gly Ala Gly Glu Leu Ala
 1185 1190 1195 1200
 20 Gly Glu Leu Ala Ser Leu Gly Ala Lys Val Thr Val Ala Ala Cys Asp
 1205 1210 1215
 Met Ala Asp Arg Glu Ala Val Arg Ala Leu Leu Asp Glu His Arg Pro
 1220 1225 1230
 25 Thr Ala Val Phe His Thr Ala Gly Thr Pro His Ser Ala Glu Phe Thr
 1235 1240 1245
 Ala Leu Asp Glu Thr Thr Thr Ala Gly Val Tyr Gly Gly Lys Val Leu
 1250 1255 1260
 Gly Ala Arg His Leu Asp Glu Leu Thr Arg Glu Leu Gly Ile Gly Leu
 1265 1270 1275 1280
 35 Asp Ala Phe Val Leu Phe Ser Ser Gly Ala Ala Val Trp Gly Ser Gly
 1285 1290 1295
 Gly Gln Thr Ala Tyr Gly Ala Ala Asn Ala Ala Leu Asp Ala Leu Ala
 1300 1305 1310
 40 Glu Arg Arg Arg Ala Ala Gly Leu Pro Ala Thr Ser Val Ala Trp Gly
 1315 1320 1325
 Leu Trp Gly Gly Gly Gly Met Gly Glu Gly Asp Gly Glu Glu Phe Leu
 1330 1335 1340
 45 Ser Arg Arg Gly Leu Gly Val Met Pro Pro Glu Asp Ala Leu Glu Ala
 1345 1350 1355 1360
 Leu Asp Arg Ala Leu Asp Arg Glu Asp Thr Thr Val Val Val Ala Asp
 1365 1370 1375
 50 Val Asp Trp Glu Arg Phe Ala Pro Ala Phe Thr Ala Phe Arg Pro Ser
 1380 1385 1390
 Ala Leu Ile Ser Arg Leu Val Ser Asp Gly Gly Glu Ala Gly Gly Gln
 1395 1400 1405
 55

Asp Ala Pro Asp Gly Thr Leu Phe Ala Ala Gly Phe Ala Ala Ala Gly
 1410 1415 1420
 5 Pro Leu Glu Arg Gln Glu Met Leu Leu Gly Leu Val Arg Arg His Val
 1425 1430 1435 1440
 Ala Ala Val Leu Gly His Pro Gly Thr Ala Asp Ile Gly Pro Asp Arg
 1445 1450 1455
 10 Ala Phe Lys Glu Leu Gly Phe Ser Ser Val Thr Ala Val Glu Leu Ala
 1460 1465 1470
 Gly Arg Leu Gly Arg Glu Cys Gly Arg Lys Leu Pro Pro Thr Leu Val
 1475 1480 1485
 15 Phe Asp His Pro Thr Ala Ala Ala Ala Val Glu His Leu Ala Glu Leu
 1490 1495 1500
 Leu Thr Pro Pro Ala Gly Pro Ala Ala Gly Pro Arg Glu Glu Glu Ala
 1505 1510 1515 1520
 Arg Ala Ala Leu Ala Arg Val Pro Leu Glu Arg Leu Arg Glu Ala Gly
 1525 1530 1535
 20 Leu Leu Asp Ala Leu Leu Arg Leu Ala Ala Asp Glu Ser Gly Ala Thr
 1540 1545 1550
 Thr Pro Arg Thr Ser Ala Ala Ser Gly Ala Pro Arg Gly Arg Glu Glu
 1555 1560 1565
 30 Pro Asp Gly Arg Gly Glu Pro Asp Gly Ser Gly His Arg Glu Ser Pro
 1570 1575 1580
 Asp Ala Ala Gly Gly Ser Asp Ala Leu Asp Asp Leu Asp Gly Asp Ala
 1585 1590 1595 1600
 35 Leu Val Arg Leu Ala Leu Gly Glu Pro Gly Glu *
 1605 1610

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1842 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

50 Met Ala Met Ser Ala Glu Arg Leu Thr Glu Ala Leu Arg Thr Ser Leu
 1 5 10 15
 Lys Glu Ala Glu Arg Leu Arg Arg Gln Asn Arg Glu Leu Arg Ala Ala
 20 25 30
 55 Arg Asp Ala Ala Arg Glu Pro Ile Ala Val Val Gly Met Ala Cys Arg
 35 40 45

Tyr Pro Gly Gly Val Thr Gly Pro Glu Glu Leu Trp Glu Leu Val Ala
 50 55 60
 5 Gly Gly Arg Asp Ala Ile Gly Pro Phe Pro Val Asp Arg Gly Trp Asp
 65 70 75 80
 Val Ala Ser Val Tyr Asp Pro Asp Pro Glu Ser Lys Gly Thr Thr Tyr
 85 90 95
 10 Cys Arg Glu Gly Gly Phe Leu Glu Gly Ala Gly Asp Phe Asp Ala Ala
 100 105 110
 Phe Phe Gly Ile Ser Pro Arg Glu Ala Leu Val Met Asp Pro Gln Gln
 115 120 125
 15 Arg Leu Leu Leu Glu Val Ser Trp Glu Ala Leu Glu Arg Ala Gly Ile
 130 135 140
 Asp Pro Ser Ser Leu Arg Gly Ser Arg Gly Gly Val Tyr Val Gly Ala
 145 150 155 160
 20 Ala His Gly Ser Tyr Ala Ser Asp Pro Arg Leu Val Pro Glu Gly Ser
 165 170 175
 25 Glu Gly Tyr Leu Leu Thr Gly Ser Ala Asp Ala Val Met Ser Gly Arg
 180 185 190
 Ile Ser Tyr Ala Leu Gly Leu Glu Gly Pro Ser Met Thr Val Glu Thr
 195 200 205
 30 Ala Cys Ser Ser Ser Leu Val Ala Leu His Leu Ala Val Arg Ala Leu
 210 215 220
 Arg His Gly Glu Cys Gly Leu Ala Leu Ala Gly Gly Val Ala Val Met
 225 230 235 240
 35 Ala Asp Pro Ala Ala Phe Val Glu Phe Ser Arg Gln Lys Gly Leu Ala
 245 250 255
 Ala Asp Gly Arg Cys Lys Ala Phe Ser Ala Ala Ala Asp Gly Thr Gly
 260 265 270
 40 Trp Ala Glu Gly Val Gly Val Leu Val Leu Glu Arg Leu Ser Asp Ala
 275 280 285
 Arg Arg Ala Gly His Thr Val Leu Gly Leu Val Thr Gly Thr Ala Val
 290 295 300
 45 Asn Gln Asp Gly Ala Ser Asn Gly Leu Thr Ala Pro Asn Gly Pro Ala
 305 310 315 320
 50 Gln Gln Arg Val Ile Ala Glu Ala Leu Ala Asp Ala Gly Leu Ser Pro
 325 330 335
 Glu Asp Val Asp Ala Val Glu Ala His Gly Thr Gly Thr Arg Leu Gly
 340 345 350
 55 Asp Pro Ile Glu Ala Gly Ala Leu Leu Ala Ala Ser Gly Arg Asn Arg
 355 360 365

Ser Gly Asp His Pro Leu Trp Leu Gly Ser Leu Lys Ser Asn Ile Gly
 370 375 380
 5 His Ala Gln Ala Ala Ala Gly Val Gly Gly Val Ile Lys Met Leu Gln
 385 390 395 400
 Ala Leu Arg His Gly Leu Leu Pro Arg Thr Leu His Ala Asp Glu Pro
 405 410 415
 10 Thr Pro His Ala Asp Trp Ser Ser Gly Arg Val Arg Leu Leu Thr Ser
 420 425 430
 Glu Val Pro Trp Gln Arg Thr Gly Arg Pro Arg Arg Thr Gly Val Ser
 435 440 445
 15 Ala Phe Gly Val Gly Gly Thr Asn Ala His Val Val Leu Glu Glu Ala
 450 455 460
 Pro Ala Pro Pro Ala Pro Glu Pro Ala Gly Glu Ala Pro Gly Gly Ser
 465 470 475 480
 20 Arg Ala Ala Glu Gly Ala Glu Gly Pro Leu Ala Trp Val Val Ser Gly
 485 490 495
 Arg Asp Glu Pro Ala Leu Arg Ser Gln Ala Arg Arg Leu Arg Asp His
 500 505 510
 25 Leu Ser Arg Thr Pro Gly Ala Arg Pro Arg Asp Ile Ala Phe Ser Leu
 515 520 525
 Ala Ala Thr Arg Ala Ala Phe Asp His Arg Ala Val Leu Ile Gly Ser
 530 535 540
 30 Asp Gly Ala Glu Leu Ala Ala Ala Leu Asp Ala Leu Ala Glu Gly Arg
 545 550 555 560
 35 Asp Gly Pro Ala Val Val Arg Gly Val Arg Asp Arg Asp Gly Arg Met
 565 570 575
 Ala Phe Leu Phe Thr Gly Gln Gly Ser Gln Arg Ala Gly Met Ala His
 580 585 590
 40 Asp Leu His Ala Ala His Thr Phe Phe Ala Ser Ala Leu Asp Glu Val
 595 600 605
 Thr Asp Arg Leu Asp Pro Leu Leu Gly Arg Pro Leu Gly Ala Leu Leu
 610 615 620
 45 Asp Ala Arg Pro Gly Ser Pro Glu Ala Ala Leu Leu Asp Arg Thr Glu
 625 630 635 640
 50 Tyr Thr Gln Pro Ala Leu Phe Ala Val Glu Val Ala Leu His Arg Leu
 645 650 655
 Leu Glu His Trp Gly Met Arg Pro Asp Leu Leu Leu Gly His Ser Val
 660 665 670
 55 Gly Glu Leu Ala Ala Ala His Val Ala Gly Val Leu Asp Leu Asp Asp
 675 680 685

Ala Cys Ala Leu Val Ala Ala Arg Gly Arg Leu Met Gln Arg Leu Pro
 690 695 700
 5 Pro Gly Gly Ala Met Val Ser Val Arg Ala Gly Glu Asp Glu Val Arg
 705 710 715 720
 Ala Leu Leu Ala Gly Arg Glu Asp Ala Val Cys Val Ala Ala Val Asn
 725 730 735
 10 Gly Pro Arg Ser Val Val Ile Ser Gly Ala Glu Glu Ala Val Ala Glu
 740 745 750
 Ala Ala Ala Gln Leu Ala Gly Arg Gly Arg Arg Thr Arg Arg Leu Arg
 755 760 765
 15 Val Ala His Ala Phe His Ser Pro Leu Met Asp Gly Met Leu Ala Gly
 770 775 780
 Phe Arg Glu Val Ala Ala Gly Leu Arg Tyr Arg Glu Pro Glu Leu Thr
 785 790 795 800
 20 Val Val Ser Thr Val Thr Gly Arg Pro Ala Arg Pro Gly Glu Leu Thr
 805 810 815
 Gly Pro Asp Tyr Trp Val Ala Gln Val Arg Glu Pro Val Arg Phe Ala
 820 825 830
 25 Asp Ala Val Arg Thr Ala His Arg Leu Gly Ala Arg Thr Phe Leu Glu
 835 840 845
 Thr Gly Pro Asp Gly Val Leu Cys Gly Met Ala Glu Glu Cys Leu Glu
 850 855 860
 Asp Asp Thr Val Ala Leu Leu Pro Ala Ile His Lys Pro Gly Thr Ala
 865 870 875 880
 35 Pro His Gly Pro Ala Ala Pro Gly Ala Leu Arg Ala Ala Ala Ala Ala
 885 890 895
 Tyr Gly Arg Gly Ala Arg Val Asp Trp Ala Gly Met His Ala Asp Gly
 900 905 910
 40 Pro Glu Gly Pro Ala Arg Arg Val Glu Leu Pro Val His Ala Phe Arg
 915 920 925
 His Arg Arg Tyr Trp Leu Ala Pro Gly Arg Ala Ala Asp Thr Asp Asp
 930 935 940
 45 Trp Met Tyr Arg Ile Gly Trp Asp Arg Leu Pro Ala Val Thr Gly Gly
 945 950 955 960
 Ala Arg Thr Ala Gly Arg Trp Leu Val Ile His Pro Asp Ser Pro Arg
 965 970 975
 50 Cys Arg Glu Leu Ser Gly His Ala Glu Arg Ala Leu Arg Ala Ala Gly
 980 985 990
 55 Ala Ser Pro Val Pro Leu Pro Val Asp Ala Pro Ala Ala Asp Arg Ala
 995 1000 1005

Ser Phe Ala Ala Leu Leu Arg Ser Ala Thr Gly Pro Asp Thr Arg Gly
 1010 1015 1020
 5 Asp Thr Ala Ala Pro Val Ala Gly Val Leu Ser Leu Leu Ser Glu Glu
 1025 1030 1035 1040
 Asp Arg Pro His Arg Gln His Ala Pro Val Pro Ala Gly Val Leu Ala
 1045 1050 1055
 10 Thr Leu Ser Leu Met Gln Ala Met Glu Glu Glu Ala Val Glu Ala Arg
 1060 1065 1070
 Val Trp Cys Val Ser Arg Ala Ala Val Ala Ala Ala Asp Arg Glu Arg
 1075 1080 1085
 15 Pro Val Gly Ala Gly Ala Ala Leu Trp Gly Leu Gly Arg Val Ala Ala
 1090 1095 1100
 Leu Glu Arg Pro Thr Arg Trp Gly Gly Leu Val Asp Leu Pro Ala Ser
 1105 1110 1115 1120
 20 Pro Gly Ala Ala His Trp Ala Ala Ala Val Glu Arg Leu Ala Gly Pro
 1125 1130 1135
 Glu Asp Gln Ile Ala Val Arg Ala Ser Gly Ser Trp Gly Arg Arg Leu
 1140 1145 1150
 25 Thr Arg Leu Pro Arg Asp Gly Gly Gly Arg Thr Ala Ala Pro Ala Tyr
 1155 1160 1165
 Arg Pro Arg Gly Thr Val Leu Val Thr Gly Gly Thr Gly Ala Leu Gly
 1170 1175 1180
 Gly His Leu Ala Arg Trp Leu Ala Ala Ala Gly Ala Glu His Leu Ala
 1185 1190 1195 1200
 35 Leu Thr Ser Arg Arg Gly Pro Asp Ala Pro Gly Ala Ala Gly Leu Glu
 1205 1210 1215
 Ala Glu Leu Leu Leu Leu Gly Ala Lys Val Thr Phe Ala Ala Cys Asp
 1220 1225 1230
 40 Thr Ala Asp Arg Asp Gly Leu Ala Arg Val Leu Arg Ala Ile Pro Glu
 1235 1240 1245
 Asp Thr Pro Leu Thr Ala Val Phe His Ala Ala Gly Val Pro Gln Val
 1250 1255 1260
 45 Thr Pro Leu Ser Arg Thr Ser Pro Glu His Phe Ala Asp Val Tyr Ala
 1265 1270 1275 1280
 Gly Lys Ala Ala Gly Ala Ala His Leu Asp Glu Leu Thr Arg Glu Leu
 1285 1290 1295
 50 Gly Ala Gly Leu Asp Ala Phe Val Leu Tyr Ser Ser Gly Ala Gly Val
 1300 1305 1310
 Trp Gly Ser Ala Gly Gln Gly Ala Tyr Ala Ala Ala Asn Ala Ala Leu
 1315 1320 1325
 55

Asp Ala Leu Ala Arg Arg Arg Ala Ala Asp Gly Leu Pro Ala Thr Ser
 1330 1335 1340
 5 Ile Ala Trp Gly Val Trp Gly Gly Gly Gly Met Gly Ala Asp Glu Ala
 1345 1350 1355 1360
 Gly Ala Glu Tyr Leu Gly Arg Arg Gly Met Arg Pro Met Ala Pro Val
 1365 1370 1375
 10 Ser Ala Leu Arg Ala Met Ala Thr Ala Ile Ala Ser Gly Glu Pro Cys
 1380 1385 1390
 Pro Thr Val Thr His Thr Asp Trp Glu Arg Phe Gly Glu Gly Phe Thr
 1395 1400 1405
 15 Ala Phe Arg Pro Ser Pro Leu Ile Ala Gly Leu Gly Thr Pro Gly Gly
 1410 1415 1420
 Gly Arg Ala Ala Glu Thr Pro Glu Glu Gly Asn Ala Thr Ala Ala Ala
 20 1425 1430 1435 1440
 Asp Leu Thr Ala Leu Pro Pro Ala Glu Leu Arg Thr Ala Leu Arg Glu
 1445 1450 1455
 25 Leu Val Arg Ala Arg Thr Ala Ala Ala Leu Gly Leu Asp Asp Pro Ala
 1460 1465 1470
 Glu Val Ala Glu Gly Glu Arg Phe Pro Ala Met Gly Phe Asp Ser Leu
 1475 1480 1485
 30 Ala Thr Val Arg Leu Arg Arg Gly Leu Ala Ser Ala Thr Gly Leu Asp
 1490 1495 1500
 Leu Pro Pro Asp Leu Leu Phe Asp Arg Asp Thr Pro Ala Ala Leu Ala
 1505 1510 1515 1520
 35 Ala His Leu Ala Glu Leu Leu Ala Thr Ala Arg Asp His Gly Pro Gly
 1525 1530 1535
 Gly Pro Gly Thr Gly Ala Ala Pro Ala Asp Ala Gly Ser Gly Leu Pro
 1540 1545 1550
 40 Ala Leu Tyr Arg Glu Ala Val Arg Thr Gly Arg Ala Ala Glu Met Ala
 1555 1560 1565
 Glu Leu Leu Ala Ala Ala Ser Arg Phe Arg Pro Ala Phe Gly Thr Ala
 45 1570 1575 1580
 Asp Arg Gln Pro Val Ala Leu Val Pro Leu Ala Asp Gly Ala Glu Asp
 1585 1590 1595 1600
 50 Thr Gly Leu Pro Leu Leu Val Gly Cys Ala Gly Thr Ala Val Ala Ser
 1605 1610 1615
 Gly Pro Val Glu Phe Thr Ala Phe Ala Gly Ala Leu Ala Asp Leu Pro
 1620 1625 1630
 55 Ala Ala Ala Pro Met Ala Ala Leu Pro Gln Pro Gly Phe Leu Pro Gly
 1635 1640 1645

Glu Arg Val Pro Ala Thr Pro Glu Ala Leu Phe Glu Ala Gln Ala Glu
 1650 1655 1660
 5 Ala Leu Leu Arg Tyr Ala Ala Gly Arg Pro Phe Val Leu Leu Gly His
 1665 1670 1675 1680
 Ser Ala Gly Ala Asn Met Ala His Ala Leu Thr Arg His Leu Glu Ala
 1685 1690 1695
 10 Asn Gly Gly Gly Pro Ala Gly Leu Val Leu Met Asp Ile Tyr Thr Pro
 1700 1705 1710
 Ala Asp Pro Gly Ala Met Gly Val Trp Arg Asn Asp Met Phe Gln Trp
 1715 1720 1725
 15 Val Trp Arg Arg Ser Asp Ile Pro Pro Asp Asp His Arg Leu Thr Ala
 1730 1735 1740
 Met Gly Ala Tyr His Arg Leu Leu Leu Asp Trp Ser Pro Thr Pro Val
 1745 1750 1755 1760
 20 Arg Ala Pro Val Leu His Leu Arg Ala Ala Glu Pro Met Gly Asp Trp
 1765 1770 1775
 Pro Pro Gly Asp Thr Gly Trp Gln Ser His Trp Asp Gly Ala His Thr
 1780 1785 1790
 25 Thr Ala Gly Ile Pro Gly Asn His Phe Thr Met Met Thr Glu His Ala
 1795 1800 1805
 Ser Ala Ala Ala Arg Leu Val His Gly Trp Leu Ala Glu Arg Thr Pro
 1810 1815 1820
 30 Ser Gly Gln Gly Gly Ser Pro Ser Arg Ala Ala Gly Arg Glu Glu Arg
 1825 1830 1835 1840
 35 Pro *

(2) INFORMATION FOR SEQ ID NO:7:

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 44377 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 45 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 350..14002
 50 (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 14046..20036
 55 (ix) FEATURE:
 (A) NAME/KEY: CDS

(B) LOCATION: 20110..31284

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 31329..36071

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 36155..41830

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

	GACCGCTCGG GGAGACCTGA CATATTCGTC GCGAAGTGGT TGTCCGCGCC GCGAGGTACT	60
15	GAAATCTTCT CCGCTCGCCC AGGACTCCGC GTGCAGGTCA CCGGAGTGGC CGACCGGCCG	120
	GGACGTCGGA GCGCCGACCC TCGGACCTG GTGCGATGCC GTGTGGTCCC GCATGATCCC	180
	GCGCGGTCTC CGGTGACGAG AATCGGTGGA CAATCTCCGA ACTTGACACA ATTGATTCTC	240
20	GTTCACCGGC CGTTCCTGTC GCGCGGCAGT TCGCCCGCTG TACGCTCGGG AAGATCAAGA	300
	AAAGGCAGAA AAGCCACGGC GTGGTACGGC GAACATATGA GGGATGCAGG TGTCTGGAGA	360
25	ACTCGCGATT TCCCGCAGTG ACGACCGGTC CGACGCCGTT GCCGTGGTCG GAATGGCGTG	420
	CCGTTTCCC GCGCGCCCGG GAATTGCCGA ATTCTGGAAA CTGCTGACCG ACGGAAGGGA	480
	CGCGATCGGC CGGGACGCCG ACGGCGCGCG GCGCGGCATG ATCGAGGCGC CCGGCGACTT	540
30	CGACGCCGCC TTCTTCGGCA TGTCACCCCG CGAGGCCGCC GAGACCGACC CCCAGCAGCG	600
	CCTGATGCTC GAACTCGGCT GGGAGGCTCT GGAGGACGCC GGCATCGTCC CCGGCTCCCT	660
	GCGGGCGGAG GCGGTGCGCG TCTTCGTGGG GGCCATGCAC GACGACTACG CCACCCTGCT	720
35	CCACCGCGCC GCGCGCGCCG TCGGCCCCCA CACCGCCACC GGCCTCCAGC GCGCCATGCT	780
	CGCCAACCGG CTCTCCTACG TCCTGGGAC GCGCGCCCCC AGCCTCGCGG TCGACACCGC	840
40	CCAGTCGTCC TCCCTGGTCG CCGTGGCCCT CGCGTCGAG AGCCTGCGGG CCGGCACCTC	900
	CCGCGTCGCC GTCGCCGGGG GCGTCAACCT GGTCTTCGCC GACGAGGGAA CGGCCGCCAT	960
	GGAACGCCTC GCGCGGCTGT CACCCGACGG CCGCTGCCAC ACCTTCGACG CCGTGCCAA	1020
45	CGGCTATGTC CCGGTGAGG GCGGCGCGC CGTCGTCCTG AAGCCCCTCG CCGACGCCCT	1080
	GGCCGACGGG GACCCCGTGT ACTGCGTGGT GCGTGGCGTC GCGTCGGCA ACGACGGCGG	1140
	CGGCCCCGGG CTGACCGCTC CCGACCGGA GGGACAGGAG GCGGTGCTCC GGGCCGCTG	1200
50	CGCCCAGGCC CCGGTGACC CCGCCGAGGT GCGTTTCGTC GAACTGCACG GCACGGGAAC	1260
	CCCGTGGGC GACCCGGTCG AGGCACACGC CCTCGGCGCG GTGCACGGCT CCGGTGCGCC	1320
	GGCCGACGAC CCCCTGCTGG TGGGGTCGGT GAAGACCAAC ATCGGCCACC TGGAGGGCGC	1380
55	CGCCGCGATC GCGGGCCTGG TCAAGGCCGC ACTGTGCCTG CGGGAACGCA CCCTTCCCGG	1440

	CTCGCTGAAC TTCGCCACCC CCTCTCCGGC CATCCCGCTG GACCAGCTCC GGCTGAAGGT	1500
5	GCAGACCGCT GCCGCCGAGC TGCCCGCTCGC CCCGGGCGGC GCACCCCTGC TGGCGGGTGT	1560
	CAGTTGGTTC GGCATCGGTG GCACCAACTG CCATGTGGTC CTGGAACACC TGCCCTCCCG	1620
	GCCCCACCCG GCCGTCTCCG TCGCCGCCTC GCTTCCGGAC GTCCCGCCGC TGTGTGTGTC	1680
10	CGCGCGGTG GAGGGGGCGT TCGGGGCGCA GCGGGTGGG TTGGGTGAGT ACGTGGAGCG	1740
	GGTGGGCGCG GATCCGCGGG ATGTGGCTTA TTCCGTGGCT TCGACCGGA CTCTTTTCGA	1800
	GCACCGTGG GTGGTGGGT GTGGTGGGG TGGGAGCTC GTCCGTGCTC TTGGTGGGTT	1860
15	TGCTGCCGGG AGGGTGTCTG GGGGTGTGCG GTCCGGGCGG GCTGTGCCGG GTGGGGTGGG	1920
	GGTGTGTGTC ACCGGTCAGG GTGCGCAGTG GGTGGGTATG GGGCGTGGGT TGTATGCCGG	1980
	GGGTGGGGTG TTTGCCGAGC TGCTGCATGA GGTGTTGTG ATGCTGGGG AGGTGCATGG	2040
20	TCGGTGGTTC CGGGATGTGA TGTTCGGCGA CGTCGACGTG GACGCGGGTG CCGGGGCTGA	2100
	TGCGGGTGCC GGTGCCGGTG CTGGGGTCCG TTCTGGTTCC GGTCTGTGG GTGGGTGTG	2160
25	GGGTCCGACG GAGTTTGCTC AGCCTGCGTT GTTTGCGTTC GAGGTGGCGT TGTTCGGGC	2220
	GTTGGAGGCT CCGGGTGTG AGGTGTGGT GGTGTTGGG CATTCGGTGG GGGAGGTGGC	2280
	TGCTGCGTAT GTGGCGGGG TGTGTGCTGT GGTGATGCG GTGCGGTTG TGGTGGCGCG	2340
30	GGGTGGGTTG ATGGGTGGG TCCCGGTGGG TGGGGGATG TGGTGGTGG GGGCGTCGGA	2400
	GTCCGTGGTG CCGGGGGTTG TTGAGGGGT GGGGGAGTG GTGTGGTTG CCGCGGTGAA	2460
	TGGGCCGCGG TCGGTGGTGT TGTGGGTGA TGTGGGTGT CTGGAGTCGG TGGTTGCCTC	2520
35	GCTGATGGG GATGGGGTGG AGTCCCGCG GTTGATGTC TCCCATGGG TTCATTGGG	2580
	GTTGATGGAG CCGGTGTGCG GGGAGTTCCG GGGGGTTGT GAGTCGTTG AGTTGGGTG	2640
40	GGTGCGGCCG GGTGTGGTGG TGTGTGCGG TGTGTGCGG GGGGTGGTG GTTCGGGGGA	2700
	GTTGGGGAT CCGGGTATT GGTGCGTCA TGCGCGGAG GCGGTGCGTT TCGCGGATG	2760
	GGTGGGGTG GTCCGTGCTC TGGGTGTGG GACGTTGGTG GAGGTGGGTC CGCATGGGT	2820
45	GCTGACGGG ATGGCGGGT AGTGCTTGG GCGCGGTGAT GATGTGGTGG TGGTGCCGGC	2880
	GATGCGCGG GCGGTGCGG AGCGGGAGG GTTCGAGCG GCGCTGGGA CCGTGTTCAC	2940
	CCGGGACGCC GGCCTGGAC CCACGGCACT CCACACCGG AGCACCGGCC GGCGCATCGA	3000
50	CCTCCCCACC TACCCCTTCC AACGCCGTAC CCACTGGTGG CCCGCGCTGA GCCGGCCGGT	3060
	CACGGCCGAC GCCGGGCGG GTGTGACCG CACCGATGCC GTGGGGCACA GCGTCTCCCC	3120
	GGACCCGAG AGCACCGAG GAGCGTCCCA CAGGGACAG GACGACGAG CGGACTCGGC	3180
55	GTCACCGAG CCGATGTCCC CCGAGGATG CGTCCGCCTG GTCCGCGAGA GCACCGCGGC	3240

	CGTCCTGGGC CACGACGATC CCGGCGAGGT CGCGCTCGAC CGCACCTTCA CCTCCCAGGG	3300
5	CATGGACTCG GTGACCGCGG TCGAGCTGTG CGACCTGCTG AAGGGCGCCT CGGGGCTCCC	3360
	CCTCGCCGCC ACGTGGTCT ACGACCTGCC CACCCCGCGT GCCGTGCGCG AGCACATCGT	3420
	GGAAGCCGCG GCGGGGCCGA AGGACTCGGT TGCCGGTGGG CCCGGAGTGC TCTCGTCGGC	3480
10	CGCGGTAGGG GTGTGCGACG CCCGGGGCGG CAGCCGGGAC GACGACGACC CGATCGCCAT	3540
	CGTGGGTGTC GGTGCCCCG TCCCCGGCGG CGTCGACTCG CGCGCCGCTC TCTGGGAGCT	3600
	GCTGGAGTCC GCGCCGACG CCATCTCGTC CTTCCCCACC GACCGCGGCT GGGACCTCGA	3660
15	CGGGCTGTAC GACCCCGAGC CCGGGACGCC CGGCAAGACC TATGTGCGGG AGGGCGGGTT	3720
	CCTGCACTCG GCGCCGAGT TCGACGCGGA GTTCTTCGGG ATATCGCCGC GCGAGGCCAC	3780
	GGCCATGGAC CCGCAGCAGC GCTTGCTGCT GGAAGCGTCG TGGGAGGCCC TCGAGGACGC	3840
20	CGGAGTGCTC CCCGAGTCAC TCGCGGGCGG CGACGCCGGA GTGTTCGTCTG GCGCCACCGC	3900
	ACCGGAGTAC GGGCCGAGGC TTCACGAGGG AGCGGACGGA TACGAGGGGT ACCTGCTCAC	3960
25	CGGCACCACC GCGAGCGTGG CCTCCGGCCG GATCGCCTAC ACCCTCGGCA CCGGGCGACC	4020
	GGCGCTCACC GTCGACACCG CGTGCTCCTC GTCCCTGGTG GCGCTGCACC TGGCCGTGCA	4080
	GGCGCTGCGC CGGGGCGAGT GCGGGCTGGC TCTGGCGGGC GCGGCCACGG TGATGTGCGG	4140
30	GCCCCGCATG TTCGTGGAGT TCTCGCGCA GCGCGGGCTC GCCCCGACG GCGCTGCAT	4200
	GCCGTCTCTC GCGATGCCG ACGGTACGGC CTGGTCCGAG GGTGTGCGCG TACTGGCACT	4260
	GGAGCGGCTC TCGACGCCC GCGGTGCGGG ACACCGGGTG CTGGGCGTGG TCGGGGCGAG	4320
35	TGCGGTCAAC CAGGACGGTG CCAGCAACGG CCTGACCGCT CCCAACCGCT CCGCGCAGGA	4380
	GGGCGTCATC CGAGCTGCCC TGGCCGACGC CGGCCTCGCG CCGGGTGACG TCGACGCGT	4440
	GGAGGCGCAC GGTACGGGA CCGCGCTGGG CGATCCGATC GAGGCGAGCG CGCTGCTGGC	4500
40	CACGTACGGG CGTGAGCGGG TGGGCGACCC CTTGTGGCTC GGGTCGCTGA AGTCCAACGT	4560
	CGGTACACCC CAGGCCGCGG CCGGGGCCGC GGGTGTGGTC AAGATGCTGC TTGCCCTGGA	4620
45	GCACGGCAGC CTGCCGCGGA CACTTCACGC GGACCGGCCC AGCACGCACG TCGACTGGTC	4680
	GTCGGGCACC GTGCCCTGC TGGCAGAGGC GCGCCGGTGG CCCCGGCGGT CGGACCGCCC	4740
	GCGCCGGGCG GCTGTGTCTG CGTTCGGGAT CAGTGGGACG AACGCGCATC TGATCATCGA	4800
50	GGAGGCGCCG GAGTGGGTG AGGACATCGA CGCGCTCGCT GCTCCTGACC GCGGTACCGC	4860
	GGACCGGGCT GCTCCGTGCG CGCTGTTGTT GTCCGCGCGG TCGGAGGGGG CGTTGCGGGC	4920
	GCAGGCGGTG CCGTTGGGTG AGTACGTGGA GCGGGTGGGT GCGGATCCGC GGGATGTGGC	4980
55	TTATTGCTG GCTTCGACGC GGACTCTTTT CGAGCACCGT GCGGTGGTGC CGTGTGGTGG	5040

	GGGTGGGGAG CTCGTCGCTG CTCTTGGTGG GTTTGCTGCC GGGAGGGTGT CTGGGGGTGT	5100
5	GCGGTCCGGG CCGGCTGTGC CCGGTGGGGT GGGGGTGTTC TTCACGGGTC AGGGTCCCA	5160
	GTGGGTGGT ATGGGGCGTG GGTGTATGC GGGGGGTGG GTGTTTGGCG AGGTGCTGGA	5220
	TGAGGTGTTC TCGATGGTGG GGGAGGTGGA TGGTCGGTCG TTGCGGGATG TGATGTTCCG	5280
10	CGACGTCGAC GTGGACCGGG GTGCCGGGGC TGATGCGGGT GCCGGTGCGG GTGCTGGGGT	5340
	CGGTTCTGGT TCCGGTTCTG TGGGTGGGTT GTTGGGTCGG ACGGAGTTTC CTCAGCCTGC	5400
	GCTGTTTCCG TTGGAGGTGG CGTTGTTCCG GCGTTGGAG GCTCGGGGTG TGGAGGTGTC	5460
15	GGTGGTGTTC GGTCAATTCG TGGGGGAGGT GGCTGCTGCG TATGTGGCGG GGGTGTGTTC	5520
	GTGGGTGAT GCGGTGCGGT TGGTGGTGGC GCGGGGTGGG TTGATGGGTG GGTGCGCGT	5580
	GGGTGGGGGG ATGTGCTCGG TGGGGGCGTC GGAGTCCGTG GTGCGGGGGG TTGTTGAGGG	5640
20	GTGGGGGAG TGGGTGTGG TTGCGGCGGT GAATGGGCCG CCGTCCGTGC TGTGTGCGGG	5700
	TGATGTGGGT GTGCTGGAGT CCGTGGTTGC CTCGCTGATG GGGGATGGGG TGGAGTGCCG	5760
25	GCGGTTGGAT GTGTCCCATG GGTTCATTC GGTGTTGATG GAGCCGGTGT TGGGGGAGTT	5820
	CCGGGGGGTT GTGGAGTCGT TGGAGTTCCG TCGGGTCCG CCGGGTGTGG TGGTGGTGTTC	5880
	GGGTGTGTCC GGTGGGGTGG TGGGTTCGGG GGAGTTGGGG GATCCGGGGT ATTGGGTGCG	5940
30	TCATGCGCGG GAGGCGGTGC GTTTCGCGGA TGGGGTGGGG GTGGTCCGTG GTCTGGGTGT	6000
	GGGACGTTG GTGGAGGTGG GTCCGCATGG GGTGCTGACG GGGATGGCGG GTGAGTGCTT	6060
	GGGGGCCGGT GATGATGTGG TGGTGGTGCC GCGGATGCGG CCGGGCCGTG CCGAGCGGGA	6120
35	GGTGTTCGAG CCGGCGCTGG CGACGGTGTT CACCCGGGAC GCCGGCCTGG ACCCCACGGC	6180
	ACTCCACACC GGGAGCACCG GCCGGCGCAT CGACCTCCCC ACCTACCCCT TCCAACCGGA	6240
40	CCGCTACTGG CTGGACCCCG TTCGCACCGC CGTGACCGGC GTCGAGCCCG CCGGCTCGCC	6300
	GGGGACGCT CCGGCCACTG AGCGGGGACG GTCGACGACG GCCGGGATCC GCTACCGCGT	6360
	CGCTTGGCAG CCGGCGGTGC TCGACCGCG CAACCCCGGG CCTGCCGGTC ATGTGCTGCT	6420
45	TCTGGCCCCG GACGAGGACA CGGCCGACTC CGGACTCGCC CCCGCGATCG CACGTGAAC	6480
	CGCCGTGCGC GGGGCCGAGG TCCACACCGT CGCCGTGCGG GTCGGTACAG GCCGGGAGGC	6540
	AGCCGGGGAC CTGTTGCGGG CCGCCGGTGA CCGTGCCGCC CGCAGCACCC GAGTTCTGTG	6600
50	GCTCGCCCCG GCCGAGCCGG ACGCGGCCGA CGCCGTGCGC CTCGTCCAGG CGCTGGGCGA	6660
	GCCGGTACCC GAAGCCCCGC TCTGGATCAC CACCCGTGAG GCGGCGGCCG TCGGCCCGGA	6720
	CGAGACCCCT TCCGTGCGGG GCGCTCAGCT GTGGGACTC GGACAGGTG CCGCGCTCGA	6780
55	ACTGGGGCGG CGCTGGGGCG GCTTGGCGGA CCTGCCCGGG AGTGCGTGC CCGCGGTGCT	6840

EP 0 791 655 A2

	CCGTACGTTT	GTCGGGGCGC	TGCTCGCCGG	GGGAGAGAAC	CAGTTTCGGG	TACGGCCCTC	6900
5	CGGCGTCCAT	GTCCGCCGTG	TGGTTCCCGC	GCCCGTCCCC	GTCCCGGCCT	CCGCTCGCAC	6960
	CGTCACCACG	GCCCCCGCCA	CCGCCGTCCG	CGAGGACGCA	CGGAACGACA	CCTCGGACGT	7020
	GGTCGTGCCG	GACGACCGGT	GGTCCTCCGG	CACCGTACTG	ATCACCGGGG	GCACCGGTGC	7080
10	CCTGGGTCCG	CAGGTGCCCC	GCAGGCTCGC	CCGGTCGGGC	GCCGCGCGTC	TGCTCCTGGT	7140
	GGGCCGGGCG	GGCGGGGCGG	GCCCCGGAGT	GGGCGAACTC	GTCGAGGAGC	TGACGGCGCT	7200
	CGGTTCCGAA	GTGGCCGTGC	AGGCCTGCGA	CGTCGCCGAC	CGGGACGCAC	TGGCCGCGCT	7260
15	CCTCGCGGGC	CTCCCCGAGG	AGCGCCCCCT	CGTCGCCGTA	CTGCACGCGG	CAGGTGTGCT	7320
	CGACGACGGT	GTGCTCGACT	CGCTCACCTC	CGACCGGGTG	GACGCCGTAC	TGCGGGACAA	7380
	GGTCACCGCC	GCCCGTCACC	TGGACGAGCT	GACCGCGGAC	CTTCCGCTCG	ACGCCTTCGT	7440
20	GCTCTTCTCC	TCCATCGTCG	GCGTGTGGGG	CAACGGAGGG	CAGGCCGTCT	ACGCGGCCGC	7500
	CAACGCCGCG	CTCGACGCCC	TGGCGCAGCG	GCGCCGGGCC	AGGGGAGCCC	GTGCCGCCTC	7560
25	GATCGCCTGG	GGGCGGTGGG	CCGGTGCCGG	AATGGCCTCC	GGAACGGCGG	CGAAGTCCTT	7620
	CGAACGGGAC	GGCGTCACGG	CCCTGGACCC	CGAGCGCGCG	CTCGACGTCC	TCGACGACGT	7680
	GGTGGGCGCC	GGCGGGACCT	CTGCCCGCAG	GACGCACGCG	GCCGGCGAGA	GCTCCCTGCT	7740
30	CGTCGCCGAC	GTGGACTGGG	AGACCTTCGT	CGGGCGTTCG	GTCACCGGCC	GTACCTGGTC	7800
	GCTCTTCGAC	GGCGTCTCCG	CCGCCCGTTC	GGCGCGTGCC	GGCCATGCCG	CGGACGACCG	7860
	TGCCGCTCTC	ACCCCAGGGA	CGCGGCCCGG	CGACGGCGCA	CCGGGCGGGA	GCGGACAGGA	7920
35	CGGGGGCGAG	GGCCGGCCGT	GGCTCTCCGT	CGGCCCTTCG	CCGGCGGAAC	GCCGTCGTGC	7980
	TCTGCTCAGC	CTGTGCGCT	CGGAGGCCGC	CGGGATCCTG	CGCCACGCCT	CGGCCGACGC	8040
	GGTCGACCCG	GAGCTGGCCT	TCCGGTCCGC	CGGGTTCGAC	TCCCTCACCG	TTCTCGAACT	8100
40	GCGTAACCGC	CTGACCGCTG	CCACCGGCCT	GAACCTGCCG	AACACGCTGC	TCTTCGACCA	8160
	CCCGACCCCC	CTCTCGCTCG	CCTCCACACT	GCACGACGAA	CTGTTCCGGT	CGACAGCGA	8220
45	GGCGGAGCCG	GCAGCGGCCG	CCCCCAGGCC	GCTCATGGCC	GACGAGCGTG	AGCCGATCGC	8280
	GATCGTGGGC	ATGGCGTGCC	GTTACCCGGG	CGGTCTGGCG	TCGCCGGACG	ACCTGTGGGA	8340
	CCTGGTGGCC	GGTGACGGGC	ACACGCTCTC	CCCGTTCCCG	GCCGACCGTG	GCTGGGACGT	8400
50	CGAGGGGCTG	TACGACCCGG	AGCCGGGGGT	GCCGGGCAAG	AGCTATGTAC	GGGAAGGCGG	8460
	GTTCTTCCGT	TCCGCGGCCG	AGTTTCGACG	CGAGTTCTTC	GGGATATCGC	CGCGCGAGGC	8520
	CACGGCCATG	GACCCGACG	AGCGGTTGCT	GCTGGAGACG	TCGTGGGAGG	CGCTGGAGCG	8580
55	GGCCGGCATC	GTTCCGGACT	CGCTGCGCGG	CACCCGGACC	GGTGTCTTCA	GCGGCATCTC	8640

	CCAGCAGGAC TACGCGACCC AGCTGGGGGA CGCCGCCGAC ACCTACGGCG GGCATGTGCT	8700
5	CACGGGGACC CTCGGCAGTG TGATCTCCCG TCGGGTTGCC TATGCGTTGG GGTTCGAGGG	8760
	GCCGGCGCTG ACGGTGGACA CGCGGTGTTT GTCGTCGTTG GTGGCGTTGC ATCTGGCGGT	8820
	GCAGTCGTTG CGGCGGGGTG AGTGTGATCT GCGGTTGGCC GGTGGGGTGA CCGTGATGGC	8880
10	GACGCCGACG GTGTTCTGTTG ACTTCTCCCG GCAGCGGGGG CTGGCGCCCG ACGGGCGGTG	8940
	CAAGGCGTTC GCGGAGGGTG CGGACGGGAC GCGGTGGGCG GAGGGTCTGC GTGTGCTGCT	9000
	GGTGGAGCGG CTTTCCGACG CGCGCCGCAA CGGTCATCGG GTGCTGGCGG TGGTGGGGG	9060
15	CAGTGGCGTC AATCAGGACG GTGCGAGCAA TGGGCTGACG GCGCCGAGTG GTCCGGCGCA	9120
	GCAGCGGGTG ATCCGTGAGG CGCTGGCTGA TCGGGGCTG GTGCCCGCCG ACGTGGATGT	9180
	GGTGGAGGCG CACGGTACCG GGACGGCGCT GGGTGATCCG ATCGAGGCGG GTCCGCTGCT	9240
20	GGCCACGTAC GGGCGGGAGC GGGTCGGCGA TCCGTGTGTTG CTCGGGTCGT TGAAGTCGAA	9300
	CATCGGGCAT GCGCAGGCGG CTGCGGGTGT GGGTGGTGTG ATCAAGGTGG TGCAGGGGAT	9360
25	GCGGCATGGG TCGTTGCCCG GGACGCTGCA TGTGGATGCG CCGTCGTCGA AGGTGGAGTG	9420
	GGCTTCGGGT GCGGTGGAGC TGCTGACCGA GACCCGGTCG TGGCCGCGGC GGGTGGAGCG	9480
	GGTGGCGCGG GCGCGGCTGT CCGCGTTCCG GGTGAGCGGG ACCAACGCCC ATGTGGTCTT	9540
30	GGAGGAAGCG CCGGCGGAGG CCGGGAGCGA GCACGGGGAC GGCCTTGAAC CTGAGCGGCC	9600
	CGACCGGTG ACGGGTCCGT TGTGCTGGGT GCTTCTGCG CGGTGCGAGG GGGCGTTCCG	9660
	GGCGCAGGCG GTGCGGTTGC GTGAGTGTGT GGAGCGGGTG GGTGCGGATC CGCGGGATGT	9720
35	GGCGGGGTG TGGGTGGTGT CCGGTGCGTC GTTCGGTGAG CGTGCGGTG TGGTGGCCCC	9780
	GGGGCGTGAG GAGTTGCTGG CCGGTCTGGA TGTGGTGGCT GCCGGGGCTC CTGTGGGTGT	9840
40	GTCTTCGGGG GCCGGTGCTG TGGTGGGGG GAGTGGCGTG CCGGGTCGTG GGGTGGGGGT	9900
	GTTGTTACAG GGTGAGGGTG CGCAGTGGGT TGGTATGGGG CGTGGGTTGT ATGCGGGGG	9960
	TGGGTGTTT GCGGAGCTC TCGATGAGGT GTTGTGGGTG GTGGGGGAGG TGGATGGTGG	10020
45	GTCGTTGCGG GATGTGATGT TCGCGGATGC TGAATCGGTT TTGGGTGGGT TGTGGGTGG	10080
	GACCGAGTTT GCTCAGCCTG CGTTGTTTGC GTTGGAGGTG GCGTTGTTCC GGGCGTTGGA	10140
	GGCTCGGGGT GTGGAGGTGT CCGTGGTGTG GGTTCATTCC GTGGGGGAGG TGGCTGCTGC	10200
50	GTATGTGGCG GGGGTGTTGT CGTTGGGTGA TCGCGTGCGG TTGGTGGTGG CGCGGGGTGG	10260
	GTTGATGGGT GGGTTGCCCG TGGTGGGGG GATGTGGTGG GTGGGGCGT CCGAGTGGGT	10320
	GGTGGGGGG GTTGTGAGG GGTGGGGGA GTGGGTGTGG GTTGGGGCGG TGAATGGGCC	10380
55	GCGGTGCGTG CTGTTGTCCG GTGATGTGGG TGTGCTGGAG TCGGTGGTTG TCACGCTGAT	10440

	GGGGGATGGG GTGGAGTGCC GCGGTTGGA TGTGTCGCAT GGGTTTCATT CCGTGTGAT	10500
5	GGAGCCGGTG TTGGGGGAGT TCCGGGGGGT TGTGGAGTCG TTGGAGTTCG GTCGGGTGCG	10560
	CCCGGGTGTG GTGGTGGTGT CCGGTGTGTC GCGTGGGGTG GTGGGTTCGG GGGAGTTGGG	10620
	GGATCCGGGG TATTGGGTGC GTCATGCGCG GGAGGCGGTG CGTTTCGCGG ATGGGGTGGG	10680
10	GGTGGTGCCT GGTCTGGGTG TGGGGACGTT GGTGGAGGTG GGTCCGCATG GGGTGCTGAC	10740
	GGGGATGGCG GGTCACTGCC TGGAGGCCGG TGATGATGTG GTGGTGGTGC CGGCGATGCG	10800
	GCGGGGCCGT CCGGAGCGGG AGGTGTTCTGA GCGGCGCTG GCGACGGTGT TCACCCGGGA	10860
15	CGCCGGCCTC GACGCCACGA CACTCCACAC CGGGAGCACC GGCCGACGCA TCGACCTCCC	10920
	CACCTACCCC TTCCAACACA ACCGCTACTG GGCAACCGGC TCAGTGACCG GTGCGACCGG	10980
	CACCTCGGCA GCGCGCGCT TCGGCCTGGA GTGGAAGGAC CACCCCTTCC TCAGCGGCGC	11040
20	CACGCCGATA GCGCGCTCCG GCGCGCTGCT CCTCACCAGC AGGGTGGGGC TCGCTGCCCA	11100
	CCCGTGGCTG GCCGACCACG CCATCTCCGG CACGGTGTG CTCCCCGAA CGGCGATCGC	11160
25	CGACCTGCTG CTGCGGGCGG TCGAGGAGGT CCGCGCCGGA GGGTTCGAGG AACTGACGCT	11220
	CCATGAGCCC CTGCTCTCTC CCGAGCGAGG CCGCCTGCAC GTCCAGGTGC TGGTCGAGGC	11280
	GGCCGACGAG CAGGGACGGC GTGCCGTGGC AGTCGCCGCA CGCCCGGAGG GCCCTGGGCG	11340
30	GGACGGTGAG GAACAGGAGT GGACCCGGCA CGCGGAAGGC GTGCTCACCT CCACCGAGAC	11400
	GGCCGTTCGG GACATGGGCT GGGCCGCCGG GGCCTGGCCG CCGCCCGGTG CCGAGCCGAT	11460
	CGACGTGAG GAGCTGTACG ACGCGTTCGC CCGGACGGC TACGGCTACG GCGCGGCTT	11520
35	CACCGCACTG TCCGGCGTGT GCGGTCTCGG CGACGAACTC TTCGCCGAGG TCGCGCGGCC	11580
	CGCGGGGGGC GCGGGCACGA CCGGTGACGG TTTGCGCGTC CACCCCGCAC TCTTCGATGC	11640
	GGCCCTCCAC CCGTGGCGGG CCGGCGGGCT GCTGCCCGAC ACGGGGGCA CCACCTGGGC	11700
40	GCGGTCTCTC TGGCAGGGCA TCGCGCTCCA CACCACCGGA GCCGAGACGC TCCGCGTCAG	11760
	ACTGGCCCCCT GCGGCCGGCG GCACCGAGTC GGCCTTCTCC GTACAGGCCG CCGACCCGGC	11820
45	GGGCACCCCG GTCTCACC TCAGCGCACT GCTGCTCCGC CCGGTGACCC TGGGGAGGGC	11880
	CGACGCGCCG CAACCGCTGT ACCGCGTCGA CTGGCAGCCG GTCGGCCAGG GGACCGAGGC	11940
	CTCCGGCGCC CAGGGCTGGA CCGTGCTCGG GCAGGCCGGG GCCGAGACGG TCGCGCAGCC	12000
50	CGCCGCCCAT GCGGACCTCA CCGCCCTGCG TACGGCTGTG GCCGCGGGG GAACACCGGT	12060
	GCCCCGGCTG GTGGTCTGT CCGCGGTGGA CACCGGCTG GACGAGGGG CCGTGCTGGC	12120
	GGACGCGAG GCTCGGGCCC GTGCGGGTGA CCGCTGGGAC GACGATCCCC TACGTGTGCG	12180
55	CCTCGGGCGC GGCCTGACCC TGGTCCGGGA GTGGGTGAG GACGAACGGT TGGCGGACTC	12240

	CCGGCTCGTC	GTCTCACC	GTGGCGGGT	GGCGCCGGT	CCCGCGATG	TGCCGGACCT	12300
5	GACAGGTGCG	CCCCTGTGGG	GGCTGCTCCG	CTCCGCGCAG	TCCGAGTATC	CGGACCGCTT	12360
	CACCCTCATC	GACGTGGACG	ATTCCCCCGA	GTCCCGTGCG	GCTCTGCCCC	GGGCTCTGGG	12420
	ATCGGCCGAG	CGACAACTCG	CCCTGCGGAC	GGGCGACGTG	CTGGCGCCGG	CCCTGGTCCC	12480
10	GATGGCCACC	CGGCCGGCGG	AGACCACTCC	AGCGACGGCG	GTCGCCTCGG	CGACAACACA	12540
	GACACAGGTC	ACCGCGCCCG	CTCCCGACGA	CCCGGCTGCG	GATGCCGTGT	TCGACCCGGC	12600
	GGGCACCGTA	CTGATCACCG	CGCGCACCGG	CGCCCTGGGA	CGGCGTGTCT	CCTCGCACCT	12660
15	CGCGCGCCGG	TACGGCGTAC	GCCACATGCT	TCTGGTCAGC	AGGCGTGGAC	CGGACGCCCC	12720
	CGAGGCCGGT	CCCCTGGAAC	GGGAACTCGC	CGGTCTCGGA	GTCACCGCCA	CCTTCCTGGC	12780
	ATGCGACCTC	ACCGACATCG	AGGCCGTACG	GAAGGCCGTC	GCCGCGGTGC	CGTCGGACCA	12840
20	CCCGCTGACC	GGTGTGGTGC	ACACCGCCGG	CGTGCTGGAC	GACGGCGCCC	TGACCGGCCCT	12900
	GACCCGGCAA	CGCCTCGACA	CCGTGCTGCG	GCCCAAGGCC	GACGCCGTGC	GGAACCTCCA	12960
25	CGAGGCGACC	CTCGACCGGC	CGCTGCGCGC	GTTCTGTCCTG	TTCTCCGCCG	CCGCCGGACT	13020
	CCTGGGCCGC	CCCGGGCAGG	CCTCCTACGC	CGCCGCCAAC	GCGGTCTCTG	ACGCGCTCGC	13080
	GGGAGCCCGC	CGCGCGGCCG	GACTGCCCGC	AGTGTCCCTG	GCGTGGGGCC	TGTGGGACGA	13140
30	GCAGACGGGC	ATGGCAGGAG	GCCTCGACGA	GATGGCCCTG	CGCGTGCTGC	GCCGGGACGG	13200
	CATCGCCGCG	ATGCCTCCGG	AGCAGGGGCT	CGAACTGCTC	GACCTGGCCC	TGACCGGACA	13260
	CCGGGACGGA	CCCGCGGTCC	TCGTCCCCCT	CCTCCTCGAC	GGCGCGGCC	TGCGCCGCAC	13320
35	GGCGAAGGAG	CGCGCGCGCG	CCACGATGTC	CCCCTTGCTG	CGCGCCCTGC	TGCCCCCGCG	13380
	CCTGCGCCGC	AGCGGTGGAG	CCGGCGCCCC	CGCGCGGCC	GACCGGCACG	GCAAGGAGGC	13440
40	GGACCCCGGT	GCGGGACGCC	TCGCAGGGAT	GGTGGCACTC	GAAGCGGCGG	AGCGTTCCGC	13500
	GGCCGTCCCT	GAGCTGGTCA	CCGAACAGGT	CGCCGAGGTC	CTCGGCTACG	CGTCGGCCGC	13560
	GGAGATCGAG	CCCGAACGAC	CCTTCGGGA	GATCGGCGTC	GACTCCCTGG	CGGCGGTGGA	13620
45	GCTGCGCAAC	CGGCTCAGCC	GTCTGGTCCG	CCTGCGGTTG	CCGACCACGC	TGTCTTCGA	13680
	CCACCCACG	CCGAAGGACA	TGGCGCAGCA	CATCGACGGG	CAGTCCCCC	GCCCGGCCGG	13740
	AGCTCGCCC	GCGGACGCAG	CGCTGGAAGG	GATCGGCGAC	CTCGCGCGGG	CGGTCCGCCCT	13800
50	GCTGGGCACG	GGCGACGCCC	GCCGGGCCGA	GGTACGAGAG	CAGCTCGTCG	GACTGCTGGC	13860
	CGCGCTCGAC	CCACCTGGGC	GGACGGGCAC	CGCCGCACCC	GGCGTCCCTT	CCGCTGCCGA	13920
	TGGCGCGGAA	CCGACCGTGA	CGGACCGGCT	CGACGAGGCG	ACCGACGACG	AGATCTTCGC	13980
55	CTTCCTGGAC	GAGCAGCTGT	GACCACACCG	TGGACCGACC	GCATGCCGAG	GAGTTGGTGG	14040

	CAGCAATGAC CGCCGAGAAC GACAAGATCC GCAGCTACCT GAAGCGTGCC ACCGCCGAAC	14100
5	TGCACCGGAC CAAGTCCCCG CTGGCCGAGG TCGAGTCGGC GAGCCGCGAG CCGATCGCGA	14160
	TCGTGGGCAT GGCGTGCCGT TACCCGGGCG GTGTGGCGTC GCCGGACGAC CTGTGGGACC	14220
	TGGTGGCAGC CGGTACGGAC GCGGTCTCCG CGTTCGCCGT CGACCGTGGC TGGGACGTGC	14280
10	AGGGGCTGTA CGACCCCGAT CCGGAGGCGG TGGGCGGTAG TTACGTGCGG GAGGGCGGGT	14340
	TCCTGCACTC GGCGGCCGAG TTCGACGCGG AGTTCTTCGG GATCTCGCCC CGTGAGGCGG	14400
	CGGCGATGGA TCCGCAGCAG CGGTTGCTGC TGGAGACGTC GTGGGAGGCG CTGGAGCGGG	14460
15	CGGGGATCGT CCCC CGCTCG CTGCGCGGCA CCCGTACCGG CGTCTTCACC GGCCTCATGT	14520
	ACGACGACTA CGGGTCGCGG TTCGACTCGG CTCGCCCGGA GTACGAGGGC TACCTCGTGA	14580
	ACGCAGCGC CGGCAGCATC GCGTCCGGTC GGGTTGCCTA TCGGTTGGGG TTGGAGGGGC	14640
20	CGGCGCTGAC GGTGGACACG GCGTGTTCGT CGTCGTTGGT GCGGTTGCAT CTGGCGGTGC	14700
	AGTCGTTCCG GCGGGGTGAG TGTGATCTGG CGTTGGCCGG TGGGGTGACG GTGATGGCGA	14760
25	CGCCGACGGT GCTCGTGGAG TTCTCGCGGC AGCGGGGGCT GCCGCCGAC GGGCGGTGCA	14820
	AGGCGTTCCG GGAGGGTCCG GACGGGACGG CGTGGGCCGA GGGTGTGGGC GTGCTGCTGG	14880
	TGGAGCGGCT CTCCGACGCC CGCCGCAATG GCCATCGGGT GCTGGCGGTG GTGCGGGGCA	14940
30	GTGCGGTCAA TCAGGACGGT GCGAGCAACG GGCTGACGGC GCCGAGTGGT CCTGCGCAGC	15000
	AGCGGGTGAT CCGTGAGGCG CTGGCCGACG CCGGGCTGAC GCCGCCGAC GTCGACCGCG	15060
	TCGAGGCGCA CGGCACCGC ACACCCTGG GCGACCCAT CGAGGCGGGT GCGTTGCTGG	15120
35	CCACCTATGG CAGTGAGCGC CAGGGCCAAG GTCCGTTGTG GTTGGGGTCG TTGAAGTCGA	15180
	ACATCGGGCA TCGCAGGCG GCTGCGGGTG TGGGTGGCGT GATCAAGGTG GTGCAGGCGA	15240
	TGCGGCATGG GTCGTTGCCG CGGACGCTGC ATGTGGATGC GCCGTCGTCG AAGGTGGAGT	15300
40	GGGCTTCGGG TGCGGTGAG CTGCTGACCG AGACCCGGTC GTGGCCGCGG CCGGTGGAGC	15360
	GGGTGCGCGG GGCCGCGGTG TCGGCGTTCG GGGTGAGCGG GACCAACGCC CATGTGGTCC	15420
45	TGGAGGAAGC GCCGGCGGAG GCCGGGAGCG AGCACGGGA CGGCCCTGAA CCCGAGCGGC	15480
	CCGACGCGGT GACGGGTCCG TTGTCTGCGG TGCTTTCTGC GCGGTCCGAG GGGGCGTTGC	15540
	GGGCGCAGGC GGTGCGGTG CGTGAGTGTG TGGAGCGGGT GGGTGCGGAT CCGCGGGATG	15600
50	TGGCGGGCTC GTTGGTGGTG TCGCGTCCGT CGTTCGGTGA GCGTGCGGTG GTGGTGGGCC	15660
	GGGGGCGTGA GGAGTTGCTG GCGGGTCTGG ATGTGGTGGC TGCCGGGGCT CCTGTGGGTG	15720
	TGTCCGGGGG CGTGTCTTCG GGGGCCGGTG CTGTGGTGGC GGGGAGTGCG GTGCGGGGTC	15780
55	GTGGGGTGGG GGTGTTGTTT ACGGGTCAGG GTCCGCAGTG GGTGGGTATG GGGCGTGGGT	15840

	TGTATGCGGG GGGTGGGGTG TTTGCCGAGG TGCTGGATGA GGTGTTGTCTG GTGGTGGGGG	15900
5	AGGTGGGGGG TTGGTCGTTG CCGGATGTGA TGTTCGGCGA CGTCGACGTC GACGCGGGTG	15960
	CCGGGGCTGA TCGGGGTGTC GGTTCGGGTG TTGGTGTGGG TGGGTGTGTG GGTCCGACCG	16020
	AGTTTGCTCA GCCTGCGTTG TTTGCGTTGG AGGTGGCGTT GTTCGGGGCG TTGGAGGCTC	16080
10	GGGGTGTGGA GGTGTCGGTG GTGTTGGGTC ATTCCGTTGG GGAGGTGGCT GCTGCGTATG	16140
	TGCCCGGGGT GTTGTCTTTG CGTGATGCGG TCGGTTTGGT GGTGGCGCGG GGTGGGTTGA	16200
	TGGGTGGGTT GCCGGTGGGT GGGGGATGT GGTCCGTGGG GGCGTCGGAG TCGGTGGTGC	16260
15	GGGGGGTTGT TGAGGGGTTG GGGGAGTGGG TGTCCGTTGC GGCGGTGAAT GGGCCCGGT	16320
	CGGTGGTGTT GTCGGGTGAT GTGGGTGTGC TGGAGTCCGT GGTTCCTTCG CTGATGGGGG	16380
	ATCGGGTCCA GTGCCGCGG TTGGATGTGT CCGATGGGTT TCATTCCGTG TTGATGGAGC	16440
20	CGGTGTTGGG GGAGTCCCG GGGGTTGTGG AGTCGTTGGA GTTCGGTCCG GTCCGCGCGG	16500
	GTGTGGTGGT GGTGTCGAGT GTGTCGGGTG GGTGGTGGG TTCGGGGGAG TTGGGGGATC	16560
25	CGGGGTATTG GGTGCGTCAT GCCCGGAGG CCGTGCGTTT CGCGGATGGG GTGGGGGTGG	16620
	TGCGTGCTCT CGGTGTGGGG ACGTTGTTGG AGGTGGTCC GCATGGGGTG CTGACGGGGA	16680
	TGGCGGTGA GTCCCTGGGG GCCCGTGATG ATGTGGTGGT GGTGCCGGCG ATGCGGCGGG	16740
30	GCCGTGCCGA GCGGGAGGTG TTCGAGGCGG CGCTGGCGAC GGTGTTTACC CCGGACGCCG	16800
	GCCTGGACGC CACGACACTC CACACCGGGA GCACCGGCCG ACGCATCGAC CTCCCCACCT	16860
	ACCCCTTCCA ACACGACCGC TACTGGCTGG CCGCCCGTC CCGCCCGAGG ACGGACGGGC	16920
35	TGTCGGCGGC GGTCTGCGC GAGGTGGAGC ACCCCCTGCT CACCGCCGCC GTGGAAGTGC	16980
	CCGGCACCGA CACCGAGGTG TGGACCGGCC GCATATCCGC TGCCGACCTG CCCTGGCTCG	17040
40	CCGACCACCT GGTGTGGGAC CGAGGCGTGG TGCCGGGGAC CGCGCTGCTG GAGACGGTGC	17100
	TCCAGGTGGG AAGCCGATC GGTCTGCCGC GCGTCCCGA ACTGGTCTTG GAGACGCCGC	17160
	TGACCTGGAC GTCGGACCGC CCGCTCCAGG TCCGGATCGT CGTGACCGCT GCCGCCACCG	17220
45	CCCCCGGGG CGCGCGTGAG CTGACCCTCC ACTCGCGGCC CGAGCCCGTG GCCGCTCCT	17280
	CGTCTCCCC GAGTCCCGCC TCTCCCGGC ACCTACGGC GCAGGAGAGC GACGACGACT	17340
	GGACCCGGCA TGCCTCAGG CTGCTCGCCC CCGCTGCCG CCTCGCCGAC GACTTCGCCG	17400
50	AGCTACCCG CGCCTGGCCC CCCGTCCGCG CCGAGCCCTT CGACCTCGCC GGTCACTACC	17460
	CGTCTTCCG AGCCGCCGA GTGCGCTACG AAGCGCCTT CCGAGGGCTG CCGCGGCAT	17520
	GGCGTCGAGG CGACGAGGTC TTCGCCGACG TACGCTGCC CGACGCGCAC GCGGTGACG	17580
55	CTGATCGTTA CCGGGTGCAC CCCGCCCTGC TCGACGCGGT GCTCCACCCG ATCGCGTCCG	17640

	TGGACCCGCT GGGCGACGGC GGGCACGGTC TGCTGCCGTT CTCCTGGACC GACGTACAGG	17700
5	GACACGGCGC CGGCGGACAC GCCCTCCGGG TACGGGTGGC GGCCGTCGAC GGC GGCGCGCG	17760
	TGTCGGTCAC CGCGCCGAC CACGCGGGCA ACCCGGTGTT ATCCGCCCCG TCCCTGGCAC	17820
	TGCGTCGTAT CACCGCGGAC CGGCTTCCCG CCGCGCCCGT CGCCCCCTCTC TACCGCGTGG	17880
10	ACTGGCTGCC GTTCCCGGGT CCGGTGCCCG TATCCGCGGG CGGCCGCTGG GCGGTCTGTCG	17940
	GACCCGAGGC CGAAGCCACG GCTGCCGGAC TGCGTGCGGT GGGCCTCGAC GTGCGTACCC	18000
	ATGCGCTCCC CCTCGGAGAG CCCCTGCCTC CGCAGGCCGG TACCGACGG GAGGTGATCA	18060
15	TCCTCGACCT GACCACCACC GCAGCCGGCC GTACGGCGTC GGACGGGGGG CGGCTCAGTC	18120
	TCCTCGACGA GGTGCGTGGC ACGGTGCCCC GGACCTCGA AGCCGTACAG GCCCGCCTCG	18180
	CCGACACCGA AACGGCCCCC GACGTCGACG TCCGTACGGC CGCGCGCCCC CGCACAGCCG	18240
20	CCCGTACAAG CCCC CGCGTG GACACCCGCA CCGGAGCCCG CACCGCTGAC GGCCCCCGGC	18300
	TCGTCTCTCT GACCCGGGGC GCGGCCGGAC CCGAGGGAGG CGCGGCCGAT CCCGCGGGTG	18360
25	CCGCTGTCTG GGGGCTCGTC CCGGTGCCCC AGGCCGAACA GCCCGGCCGC TTCACCTGG	18420
	TGGACGTCGA CGGCACCCAG GCGTCGCTGC GGGCCCTGCC CCGTCTGCTG GCCACGGATG	18480
	CCGCCAGTC GGCCGTGCGC GACGGACGTG TCACCGTCCC GCGCCTCGTC CCGGTGGCCG	18540
30	ACCCCGTCCC CCACGGCGGC GGCACGGCGG CCGACGGGAC GGTGCGCGC GAGCCGTCCG	18600
	CGACCTGGA CCCC GAAGGC ACCGTGCTGA TCACCGCGG CACCGGAGCA CTGGCCGCGG	18660
	3AAACGCCCC GCACCTGGTC GACCGGCACA AGGTGCGCCA TCTCTGCTG GTGGGACGGC	18720
35	GCGTCCCGA CGCACCCGGC GTCGATCGAC TGGTGCGCGA GTTGACCGAG TCGGGTGGCG	18780
	AGGTGCGCGT ACGGGCCTGT GACGTACCG ACCCGGACGC CTTGCGCCGC CTGCTCGACG	18840
	CACTCCCCGA CGAACACCCG CTGACCTGGT TGGTGCACAC CGCCGGGGTG CTCGACGACG	18900
40	GCGTGCTCTC CGCCAGACG GCCGAGCGGA TCGACACGGT GCTCCGGCCC AAGGCCGACG	18960
	CGCCGTCCA CCTGGACGAG CTGACCCGGG AGATCGGACG GGTGCCCCTG GTGCTGTACT	19020
45	CCTCGGTCTC GGCCACCTG GGCAGCGCGG GGCAGGCCGG GTACGCGCGG GCCAACGCCT	19080
	TCATGGACGC GCTGGCCGCC CGGCGGTGGC CCGCCGGGCA CCCC CGCTG TCGCTCGGCT	19140
	GGGGCTGGTG GTCCGGGGTG GGTCTCGCCA CCGACTGGA CGGAGCGGAC GCGGCGGGG	19200
50	TCAGGCGCTC GGTCTCGCC CCGTCTGACG CCGGCGCCGC ACTGGACCTG CTCGACCGGG	19260
	CGCTGACCCG GCCCGAGCCG GCCCTGCTGC CCGTGCGGCT CGACCTGCGC GCCGCGGCCG	19320
	GTGCCACCGC TCTCCGGAG GTCTGCGTG ACCTGGCCGG CGTACCGCG GACGCCCCGA	19380
55	GCACGCCCGG GGCCGCGCG GGCACCGGGG ACGAGGACGG TGCCGTGCGC CCTGCCCCCG	19440

	CCCCGGCCGA CGCCGCCGGG ACCTGCGCCG CGCGGCTCGC GGGACGTTCC GCACCCGAGC	19500
5	GTACGGCTCT CCTGCTCGAC CTGGTGCGGA CCGAGGTCGC GCGGGTGCTC GGACACGGCG	19560
	ACCCCGCCGC GATCGGCGCC GCCCGCACCT TCAAGGACGC CGGATTTCGAC TCCCTCACCG	19620
	CTGTGACCT CCGCAACCGG CTGAACACAC GCACCGGACT GCGGCTGCCC GCGACCTCG	19680
10	TCTTCGACCA CCCACACCG CTGCCCCTCG CCGAACTCCT GCTCGACGGG CTGGAGGCGG	19740
	CCGGTCCAGC GGAACCGGCC GCTGAGGTCC CGGACGAAGC GGCCGGTGCC GAGACCCTGT	19800
	CCGGCGTGAT CGACCGGCTG GAACGCAGCC TCGCCGCGAC CGACGACGGC GACGCCCGGG	19860
15	TCCGCGCGGC ACGCGGGCTG CGCGGCCTGC TGGACGCGCT CCCC GCCGGT CCGGTTGCCG	19920
	CGTCCGGTCC GGATGCCGGA GAGCACGCCC CCGGTCGCGG CGACGTGGTG ATCGACCGGC	19980
	TCAGGTGGGC CTCGACGAC GACTTGTTTC ACCTGCTCGA CAGCGACTTC CAGTGAGCCG	20040
20	GACCGCGCCG CGCGCCGACC GCTGAACCGC TCTTCACCCA GACCCACGAG ACCACGCCTG	20100
	AGGAGAACCG TGTCTGCGAC CAACGAGGAG AAGTTGCGGG AGTACCTGCG GCGCGCGATG	20160
	GCCGACCTGC ACAGCGCACG AGAGCGGTTG CGCGAGGTCG AGTCGCGGAG CCGTGAGCCG	20220
25	ATCGCGATCG TGGGCATGGC GTGCCGTTAC CCGGGCGGTG TGGCGTCGCC GGAGGAGCTG	20280
	TGGGACCTGG TGGCCGCCGG TACGGACGCG ATCTCCCCGT TCCCGTCTGA CCGCGGCTGG	20340
30	GACGCCGAGG GTCTGTACGA CCCGGAGCCG GGGGTGCGCG GCAAGAGCTA CGTGCGCGAG	20400
	GGCGGGTTCC TGACTCGGC GGCCGAGTTC GACGCGAGT TCTTCGGGAT CTCGCCCGCT	20460
	GAGGCGGCGG CGATGGATCC GCAGCAGCGG TTGCTGCTGG AGACGTCTGT GGAGGCGCTG	20520
35	GAGCGGGCCG GGATCGTCCC CGCGTCGCTG CGCGGCACCC GTACCGGCGT CTTACCCGGC	20580
	GTCATGTACC ACGACTACGG CAGCCACCAG GTCCGCACCG CCGCCGATCC CAGTGGACAG	20640
	CTCGGCCTCG GCACCGCGGG GAGCGTCGCC TCGGGCGGGG TGGCGTACAC CCTCGGTCTA	20700
40	CAGGGGCCGG CCGTGACCAT GGACACGGCA TGCTCGTCCT CGCTGGTGCC GTTGACCTG	20760
	GCGGTGCACT CGTTGCGCGG GGGCGAGTCC GATCTCGCGT TGGCCGGCGG GCGGACGGTC	20820
45	TTGGCGACGC CCACGGTGT CTGAGGTTTC TCGCGCAAC GGGGGCTGGC GCGGACGGA	20880
	CGGTGCAAGG CGTTGCGCGA GGGCGCGGAC GGCACGGCGT GGGCCGAGGG CGCCGGTGTG	20940
	CTGCTGGTGG AGCGGCTCTC CGACGCCCGC CGCAACGGCC ATCGGGTGCT CGCGGTGGTG	21000
50	CGGGGCAGCG CCGTCAACCA GGACGGTGCC AGCAACGGCC TCACCGCACC CAGCGGGCCC	21060
	GCCCAGCAGC GGGTGATCCG TGACGCGCTG GCCGACGCGG GGCTGACGCC CGCCGACGTG	21120
	GACGCGGTG AGGCGCACGG CACCGGCACA CCGCTCGGCG ACCCGATCGA GGCCGGCGCG	21180
55	CTGATGGCCA CCTACGGCAG TGAACGGGTG GGGGACCGC TGTGGCTGGG TTCGCTGAAG	21240

	TCGAACATCG	GACACACCCA	GGCCGCCGCC	GGAGCCGCCG	GCGTCATCAA	GATGGTGCAG	21300
5	GCGTTACGGC	AGTCCGAGCT	GCCGCGCACC	CTGCACGTCT	ACGCGCCCTC	GGCCAAGGTC	21360
	GAATGGGACG	CGGGCGCCGT	GCAACTGCTC	ACCGGCGTCC	GGCCATGGCC	CCGGCGCGAG	21420
	CACAGGCCCC	GGCGGGCCGC	GGTCTCCGCC	TTCGGCGTCA	GCGGCACCAA	CGCCCACGTC	21480
10	ATCATCGAGG	AACCGCCCCG	GGCCGGTGAC	ACCTCGCCCG	CCGGCGACAC	CCCTGAGCCG	21540
	GGCGAGGCGA	CCCGCTCCCC	CTCCACCGCG	GCCGGGCCGT	CGTCCCCCTC	CGCGGTGGCC	21600
	GGGCGCTGT	CCCCCTCCTC	CCCGGCCGTG	GTCGTGCCCC	TGTCCGCCGA	GACCGCCCCC	21660
15	GCCCTGCGCG	CCCAGGCCGC	CCGCCTGCGG	GCGCACCTCG	AACGCCTCCC	CGGCACCTCG	21720
	CCGACCGACA	TCGGCCACGC	CCTGGCCGCC	GAACGCGCCG	CCCTCACCCG	ACGCGTCGTG	21780
	CTGCTCGGCG	ACGACGGAGC	CCCGGTTCGAC	GCACTCGCCG	CCCTCGCCGC	CGGCGAGACC	21840
20	ACCCCCGACG	CCGTCCACGG	CACCGCGGCG	GACATCCGCC	GGGTGCGCTT	CGTGTTCCCC	21900
	GGCCAGGGTT	CCCAGTGGGC	CGGGATGGGC	GCCGAAGTGC	TGGACACGGC	CCCGGCCTTC	21960
25	GCCGCCGAAC	TGGACCGCTG	CCAGGGCGCG	CTCTCCCCGT	ACGTGGACTG	GAACCTCGCG	22020
	GACGTGCTGC	GCGGCGCGCC	CGCGGCGCCC	GGCCTCGACC	GGGTGACGCT	CGTCCAGCCG	22080
	GCCACCTTCG	CCGTATGGT	GGGACTCGCC	GCGCTGTGGC	GCTCCCTCGG	GGTCGAACCC	22140
30	GCCGCCGTCA	TCGGCCACTC	CCAGGGCGAG	ATCGCCGCGG	CCTGCGTGGC	GGGCGCGCTC	22200
	TCCCTGGAGG	ACGCCGCCCC	GATCGTGGCC	CTCGCTCCCC	AGGTCATCGC	CCGCGAAGTC	22260
	GCCGGGCGGG	GCGGCATGGC	CTCGGTGGCC	CTGCCCGCGG	CGGAGGTCTGA	GGCCCCGCTG	22320
35	GCCGGCGGCG	TCGAGATCGC	CGCCGTCAAC	GGCCCCGGCT	CGACCGTCGT	CTGCGGAGAG	22380
	CCCGGCGCCC	TGGAGGCGTT	GCTCGTCACG	CTGGAGAGCG	AAGGCACCCG	GGTCCGCGCG	22440
	ATCGACGTCT	ACTACGCGTC	CCACTCCCAC	TACGTGAGAG	GCATCCGGGC	GGAAGTCCGC	22500
40	ACCGTCCTCG	GCCCCGTCCG	GCCGCGGAGG	GGCGACGTGC	CCTTCTACTC	CACCGTCGAG	22560
	GCGGCGCTCC	TCGACACCGC	CACCTGGAC	GCCGACTACT	GGTACCGCAA	CCTGCGCCTC	22620
45	CCGGTGCCT	TCGAGCCGAC	CGTACGCGCC	ATGCTCGACG	ACGGCGTCTGA	CGCGTTCGTG	22680
	GAGTGCTCCG	CGCATCCCGT	CCTGACCGTC	GGCGTGCGCC	AGACCGTCTGA	GAGCGCCGGC	22740
	GGCGCGGTCC	CGGCCCTCGC	TTCGCTGCGC	GCGGACGAGG	GCGGGCTGCG	GCGCTTCCTC	22800
50	ACCTCCGCGG	CCGAGGCCCA	GGTCGTCCGC	GTCCCCGTGG	ACTGGGCGAC	GCTCCGCCCA	22860
	GGCGCCGGCC	GGGTGGACCT	GCCGACCTAC	GCCTTCCAGC	GCGAACGCCA	CTGGGTCCGC	22920
	CCCGCCCGGC	CCGACTCCGC	GCGGACGGCC	GCCACGACCG	GTGACGACGC	CCCGGAGCCC	22980
55	GGAGACCGGC	TCGGCTACCA	CGTCGCGTGG	AAGGGACTGC	GCTCCACCAC	CGGCGGCTGG	23040

EP 0 791 655 A2

	CGCCCCGGCC	TGCGCCTGCT	GATCGTGCCC	ACCGGGGACC	AGTACACCGC	CCTCGCCGAC	23100
5	ACCCTGGAAC	AGGCGGTGCG	CTCCTTCGGC	GGAACGGTCC	GCCGCGTCGC	CTTCGACCCG	23160
	GCACGCACCG	GACGCGCCGA	GCTGTTCGGC	CTGCTCGAGA	CGGAGATCAA	CGGCGACACC	23220
	GCCGTCACCG	GCGTCGTCTC	GCTGCTCGGA	CTGTGCACCG	ACGGCAGGCC	GGACCACCCC	23280
10	GCCGTGCCCC	TCGCCGTAC	CGCCACCCTC	GCCCTCGTCC	AGGCCCTGGC	CGACCTCGGC	23340
	AGCACCGCAC	CGCTGTGGAC	CGTCACCTGC	GGCGCGGTGC	CCACCGCCCC	CGACGAACCTG	23400
	CCGTGCACCG	CCGGTGCCCA	GCTGTGGGGC	CTGGGCCGGG	TGGCCGCGCT	GGAGCTGCCC	23460
15	GAGGTGTGGG	GCGGCCTCAT	CGACCTTCCC	GCGCGGCCCG	ACGCCCGGGT	CCTGGACCGT	23520
	CTCGCCGGCG	TCCTCGCCGA	ACCCGGCGGC	GAGGACCAGA	TCGCCGTACG	GATGGCGGGC	23580
	GTCTTCGGCC	GCCGGGTCTT	GCGGAACCCG	GCCGACTCCC	GGCCCCCGGC	CTGGCGCGCC	23640
20	CGGGGCACCG	TCCTCATCGC	CGGCGACCTC	ACGACGGTGC	CCGGCCGACT	GGTCCGGTCC	23700
	CTCCTCGAGG	ACGGCGCCGA	CCGCGTGGTG	CTGGCCGGAC	CCGACGCCCC	CGCACAGGCC	23760
25	GCCGCCGCGC	GACTGACCGG	CGTCTCCCTC	GTCCCCGTGC	GCTGCGACGT	CACCGACCGC	23820
	GCCGCACTGG	CCGCGCTGCT	CGACGAGCAC	GCGCCACCG	TCGCCGTGCA	CGCCCCGCCC	23880
	CTGGTGCCCC	TGGCGCCGCT	GCGGGAGACG	GCACCCGGCG	ACATCGCCGC	CGCCCTCGCC	23940
30	GCCAAGACCA	CGGCCGCCGG	CCACCTGGTC	GACCTGGCGC	CGGCCCGGGG	CCTCGACGCG	24000
	CTGGTGCTGT	TCTCCTCGGT	CTCCGGAGTG	TGGGGCGGGG	CGGCCCAGGG	CGGCTACGCG	24060
	GCCGCCAGCG	CGCACCTCGA	CGCGCTGGCC	GAACGCGCCC	GCGCCGCGGG	GGTGCCCCGCG	24120
35	TTCTCCGTGG	CCTGGAGCCC	CTGGGCCGGA	GGCAGCCCCG	CCGACGGTGC	CGAGGCGGAG	24180
	TTCTCAGCC	GGCGCGGGCT	GGCTCCCTTC	GACCCCGACC	AGGCGGTGCG	GACCCTGCGC	24240
	CGCATGCTGG	AGCGCGGCAG	CGCCTGCGGT	GCGGTGCGCG	ACGTGAGTGC	GAGCCGGTTC	24300
40	GCCGCCCTCT	ACACCTGGGT	GCGTCCCGCC	GTACTCTTCG	ACGACATCCC	GGACGTGCAG	24360
	CGGCTGCGCG	CGGCCGAAC	CGCCCGAGC	ACCGGAGACT	CGACCACCTC	CGAACTCGTC	24420
45	CGCGAGCTGA	CCGCGCAGTC	CGGCCACAAG	CGGCACGCCA	CCCTGCTGCG	GCTGGTGCGC	24480
	GCACACGCCG	CCGCCGTCTT	CGGACAGTCC	TCCGGCGACG	CGGTGAGCAG	CGCCCGCGCC	24540
	TTCCGCGACC	TCGGCTTCGA	CTCGTGACCC	GCCCTCGAAC	TGCGCGACCG	GCTCAGCACC	24600
50	AGCACCGGGC	TCAAACCTGCC	CACCTCCCTG	GTCTTCGACC	ACTCCAGCCC	GGCCGCGCTC	24660
	GCCCGGCACC	TCGGTGAGGA	ACTCCTCGGC	CGGAACGACA	CCGCCGACCG	GGCCGGCCCC	24720
	GACACCCCGG	TACGGACGGA	CGAGCCCATC	GCCATCATCG	GCATGGCCTG	CCGGCTGCCC	24780
55	GGCGGGGTGC	AGTCCCCCGA	GGACCTGTGG	GACCTGCTGA	CCGGTGGGAC	CGACGCCATC	24840

EP 0 791 655 A2

	ACCCCCCTTC	CGACCAACCG	GGGATGGGAC	AACGAGACCC	TCTACGACCC	CGACCCCGAC	24900
5	TCGCCCCGGC	ACCACACCTA	CGTGCGCGAG	GGCGGGTTCC	TGCACGACGC	GGCCGAGTTC	24960
	GACCCCGGCT	TCTTCGGCAT	CAGCCCCCGC	GAGGCCCTGG	CCATGGACCC	GCAGCAGCGG	25020
	CTGATCCTGG	AGACGTCCTG	GGAGTCCTTC	GAACGGGCGG	GCATCGACCC	GGTCGAAC TG	25080
10	CGCGGCAGCC	GCACCGGGGT	CTTCGTCCGC	ACCAACGGAC	AGCACTACGT	GCCGCTCCTC	25140
	CAGGACGGCG	ACGAGAACTT	CGACGGCTAC	ATCGCCACCG	GCAACTCCGC	CAGCGTGATG	25200
	TCCGGCCGGC	TCTCCTACGT	CTTCGGACTG	GAGGGCCCCG	CCGTCACCGT	CGACACCGCC	25260
15	TGCTCGGCCT	CCCTGGCCGC	ACTGCACCTG	GCGGTGCAGT	CACTGCGCCG	CGGCGAATGC	25320
	GACTACGCCC	TCGCCGGCGG	GGCCACGGTG	ATGTCCACCC	CCGAGATGCT	GGTGGAGTTC	25380
	GCCCCGTCAGC	GAGCGGTGTC	GCCGGACGGC	CGCAGCAAGG	CGTTCCGCGA	GGCGGCCGAC	25440
20	GGGGTCGGTC	TCGCCGAGGG	AGCCGGGATG	CTGCTCGTGG	AGCGGCTGTC	GGAGGCGCAG	25500
	AAGAAGGGCC	ATCCGGTACT	GGCGGTGGTG	CGGGGCACTG	CCGTCAACCA	GGACGGTGCC	25560
25	AGCAACGGCC	TCACCGCACC	CAGCGGGCCC	GCCCAGCAGC	GGGTGATACG	GGAGGCGCTG	25620
	GCCGACGCGG	GGCTGACGCC	CGCCGACGTG	GACGCGGTGG	AGGCGCACGG	CACCGGCACG	25680
	CCGCTCGGCG	ACCCCATCGA	GGCCGGCGCG	CTGCTCGCCA	CGTACGGCCG	GGACCGGCGC	25740
30	GACGGCCCCG	TGTGGCTGGG	TTCGCTGAAG	TCGAACATCG	GGCACACCCA	GGCCGCCGCC	25800
	GGCGTGCCCG	GGGTGATCAA	GATGGTGCTG	GCGCTGCGCC	ACGGCGAGCT	GCCGCGCACC	25860
	CTGCACGCGT	CGACGGCGTC	GTCCAGGATC	GATTGGGACG	CGGGCGCCGT	GGAGTTGCTG	25920
35	GACGAGGCCA	GGCCCTGGCT	CCAGCGGGCC	GAGGGGCCGC	GCCGGGCGGG	CATCTCCTCG	25980
	TTCCGGCATCA	GCGGCACCAA	CGCGCACCTC	GTCATCGAGG	AGCCGCCGGA	GCCCACCGCG	26040
	CCCGAACTGC	TCGCGCCCGA	ACCGGCCGCC	GACGCGGACG	TCTGGTCCGA	GGAGTGGTGG	26100
40	CACGAGGTGA	CCGTGCCCCCT	GATGATGTCC	GCGCACAACG	AAGCCGCCCT	GCGCGACCAG	26160
	GCGCGGCGCC	TGCGCGCCGA	CCTGCTCGCC	CACCCCGAGC	TGCACCCGGC	CGACGTCCGC	26220
45	TACACCCTCA	TCACCACCCG	CACCCGGTTC	GAGCAGCGGG	CCGCCGTCTG	CGGCGAGAAC	26280
	TTACCGGAGC	TGATCGCGGC	CCTCGACGAC	CTCGTCGAAG	GCCGACCGCA	CCCGCTCGTG	26340
	CTGCGGGGCA	CCGCCGGCAC	CTCCGACCAG	GTCGTGTTTC	TCTTCCCCGG	CCAGGGCTCG	26400
50	CAGTGGCCCC	AGATGGCCGA	CGGGCTGCTG	GCCCCGTCCA	GCGGCTCCGG	CTCCTTCCTG	26460
	GAGACCGCCC	GCGCCTGCGA	CCTCGCGCTC	CGGCCCCACC	TCGGCTGGTC	CGTCCTGGAC	26520
	GTA CTGCGCC	GGGAACCCGG	CGCGCCCTCG	CTCGACCGGG	TCGACGTGGT	GCAGCCCGTG	26580
55	CTGTTACCA	TGATGGTCTC	GCTCGCCGAG	ACGTGGCGTT	CGCTGGGCGT	CGAACCGGCC	26640

EP 0 791 655 A2

	GCGGTCGTCG	GTCACTCCCA	GGGCGAGATC	GCCGCCGCCT	ACGTCGCCGG	CGCCCTGACG	26700
5	CTGGACGACG	CGGCGCGCAT	CGTCGCCCTG	CGCAGCCAGG	CGTGGCTGCG	GCTGGCCGGC	26760
	AAGGGCGGCA	TGGTCGCCGT	GACCCTGTCC	GAACGCGACC	TGCGTCCCCG	CCTGGAGCCC	26820
	TGGAGCGACC	GGCTCGCCGT	CGCCGCCGTC	AACGGCCCCG	AGACCTGCGC	CGTCTCCGGG	26880
10	GACCCGGACG	CCCTGGCGGA	GCTGGTCGCC	GAACTCGGTG	CGGAGGGCGT	GCACGCCCGC	26940
	CCCATCCCCG	GCGTCGACAC	CGCCGGGCAC	TCGCCGAGG	TCGACACGCT	GGAGGCCAC	27000
	CTCGGAAGG	TGCTCGCGCC	CGTCGCGCCC	CGCACCTCCG	ACATCCCGTT	CTACTCGACG	27060
15	GTCACCGGAG	GACTGATCGA	CACCGCCGAG	CTGGACGCCG	ACTACTGGTA	CCGCAACATG	27120
	CGCGAGCCGG	TGGAGTTCTG	GCAGGCCACC	CGCGCCCTGA	TCGCCGACGG	CCACGACGTG	27180
	TTCTGGAGT	CGAGCCCGCA	CCCCATGCTG	GCCGTCTCCC	TCCAGGAGAC	GATCAGCGAC	27240
20	GCCGGTTCCC	CGGCGGCCGT	CCTCGGCACC	CTGCGGCGCG	GCCAGGGCGG	CCCCCGCTGG	27300
	CTGGGCGTCG	CCCTCTGCCG	CGCCTACACC	CACGGCCTGG	AGATCGACGC	CGAGGCCATC	27360
25	TTCGGCCCCG	ACTCACGCCA	GGTGGAACTG	CCCACGTACC	CCTTCCAGCG	CGAGCGCTAC	27420
	TGGTACAGCC	CCGGCCACCG	CGGTGACGAC	CCCGCCTCCC	TCGGTCTGGA	CGCCGTCGAC	27480
	CACCCGCTGC	TGGGCAGCGG	CGTCGAACTG	CCGGAGTCCG	GTGACCGGAT	GTACACCGCA	27540
30	CGGCTGGGCG	CCGACACCAC	CCCGTGGCTG	GCCGACCACG	CGCTGCTGGG	GTGCGCGCTG	27600
	CTGCCCGGCG	CCGCCTTCGC	CGACCTGGCG	CTCTGGGCGG	GCCGCCAGGC	CGGCACCGGC	27660
	CGCGTCGAGG	AGCTCACCCT	GGCCGCGCCC	CTGGTGCTGC	CCGGCTCCGG	GGGTGTCCGG	27720
35	CTCGGGCTGA	ACGTCGGCGC	CCCGGGCACC	GACGACGCCC	GCCGCTTCGC	CGTGCACGCC	27780
	CGCGCCGAGG	CGCCACCGGA	CTGGACCCTG	CACGCCGAGG	GGTGCTCAC	CGCGCAGGAC	27840
40	ACGGCCGACG	CGCCGGACGC	CTCGGCGGCC	ACCCCGCCCC	CCGGCGCCGA	ACAACTGGAC	27900
	ATCGGCGACT	TCTACCAGCG	CTTCTCCGAA	CTCGGTTACG	GCTACGGCCC	GTTCTTCCGG	27960
	GGACTGGTGA	GCGCCCACCG	CTGCGGCCCC	GACATCCACG	CGGAGGTGCG	GCTGCCCGTC	28020
45	CAGGCGCAGG	GCGACGCGGC	CCGCTTCGGC	ATCCATCCCC	CGCTGCTGGA	CGCGGCGCTG	28080
	CAGACCATGA	GCCTCGGGGG	CTTCTTCCCC	GAGGACGGCC	GCGTCCGCAT	GCCGTTCCGC	28140
	CTGCGCGGCG	TTCGGCTGTA	CCGCGCCGGA	GCCGACCGGC	TGCACGTGCG	CGTCTCGCCC	28200
50	GTCTCCGAGG	ACGCGGTCCG	CATCAGGTGC	GCCGACGGCG	AGGGACGGCC	GGTCGCCGAG	28260
	ATCGAGTCCT	TCATCATGCG	GCCGGTCGAC	CCGGGACAGC	TCCTGGGCGG	CCGCCCGGTC	28320
	GGCGCOGACG	CGCTCTTCCG	CATCGCCTGG	CGGGAACTCG	CCGCCGGCCC	GGGCACCCGT	28380
55	ACCGGCGACG	GCACCCCTCC	CCCGGTGCGC	TGGGTGCTGG	CGGGACCCGA	CGCGCTGGGC	28440

EP 0 791 655 A2

	CTGGCCGAGG CGGCCGACGC CCACCTGCCC GCCGTTCCCG GCCCGGACGG CGCACTGCCG	28500
5	TCCCCGACGG GACGCCCCGC GCCGGACGCC GTCGTGTTCCG CGGTCCGTGC CGGGACCGGC	28560
	GACGTGCGCG CCGACGCGCA CACCGTGGCC TGCCGGGTGC TGGACCTCGT CCAGCGCCGG	28620
	CTCGCGGCCC CGGAGGGCCC GGACGCGCC CGCCTGCTGG TGGCCACCCG CGGCGCGGTC	28680
10	GCCGTACGCG ACGACGCCGA GGTGGACGAC CCGGCCGCGG CCGCCGCGTG GGGCCTGCTG	28740
	CGCTCCGCGC AGGCCGAGGA GCCCGGCCGG TTCTGCTCG TGGACCTGGA CGACGACCCG	28800
	GCGTCCGCCC GGGCGCTGAC CGACGCCCTC GCCTCCGGCG AACCGCAGAC CGCGGTCCGG	28860
15	GCCGGGACGG TGTACGTGCC CCGGCTGGAG CGGGCCGCGG ACCGCACGGA CGGGCCGCTC	28920
	ACCCCGCCCC ACGACGGTGC CTGGCGGCTG GGC CGGGCA CCGACCTCAC CCTCGACGGC	28980
	CTCGCCCTGG TGGCCGCCCC GGACGCCGAG GCGCCGCTGG AGCCCGGCCA GGTGCGCGTC	29040
20	GCCGTACGCG CCGCGGGCGT CAACTTCCGC GACGCCCTCA TCGCCCTCGG CATGTACCCG	29100
	GGCGAGGCGG AGATGGGAAC GGAGGGCGCC GGCACCGTCG TCGAGGTCCG CCCC GGCGTC	29160
25	ACCGGTGTCG CCGTCGGCGA CCGCGTGCTC GGCCTGTGGG ACGGCGGCCT GGGCCCGCTG	29220
	TGCGTGCGCG ACCACCGGCT GCTCGCCCCC GTCCCGGACG GCTGGTCCTA CGCCAGGCC	29280
	GCCTCGGTCC CCGCGGTGTT CCTCAGCGCC TACTACGGTC TGGTCACCCT GGCCGGCCTC	29340
30	AGGCCGGGGG AGCGGGTGCT CGTGACGCC GCCCGCGGG GCGTCGGCAT GGCCCGGTG	29400
	CAGATCGCCC GCCACCTCGG CGCGGAGGTG CTGGCCACCG CGAGCCCCGG CAAGTGGGAC	29460
	GCCCTGCGCG CCATGGGCAT CACCGACGAC CACCTCGCCT CCTCCGCAC CCTCGACTTC	29520
35	GCGACCGCCT TCACCGGAGC GGACGGCAGC TCCCGCGCGG ACGTCGTCTT GAACTCGCTC	29580
	ACCAAGGAGT TCGTGACGC CTCCCTCGGG CTGCTCCGTC CGGGCGGCCG GTTCCTGGAG	29640
40	CTGGGCAAGA CCGACGTCCG GGACCCCGAG CGGATCGCG CCGAACACCC CGGGGTGCGC	29700
	TACCGGGCGT TCGACCTCAA CGAGGCCGGA CCCGACGCAC TCGGCCGGCT GCTGCGGGAA	29760
	CTGATGGACC TGTTCGCCCG CGGCGTGCTG CACCGGCTGC CCGTCGTCAC CCACGACGTG	29820
45	CGCCGGGCCG CGGACGCCCT GCGACCATC AGCCAGGCC GGCACACCG AAAGCTCGTC	29880
	CTGACCATGC CGCCGCGCTG GCACCCGTAC GGCACGGTCC TGGTCACCGG TGGACCGGC	29940
	GCCCTCGGCA GCCGCATCGC CCGCCACCTG GCGAGCCGGC ACGGCGTCCG CCGGCTGCTG	30000
50	ATCGCCGCCC GCCGGGGCCC GGACGGCGAG GCGCCGCGG AGCTGGTCGC CGACCTCGCC	30060
	GCCCTGGGCG CGTCGGCCAC CGTGGTCCG TCGACGTCT CCGACCGGA CGCCGTCCGC	30120
	GGACTGCTCG CCGGCATACC GGCCGATCAC CCGTGACGG CCGTGGTGCA CAGCACCAGC	30180
55	GTCTCGACG ACGGCGTGCT GCCCGGGCTC ACCCCGAGC GGATCGGGCG CGTGCTGCGG	30240

EP 0 791 655 A2

	CCCCAAGGTGG AGGCCCGCCGT CCACCTGGAC GAACTCACCC GCGACCTCGA CCTGTCGGCG	30300
5	TTCGTCCTCT TCTCCTCCAG CGCCGGTCTG CTGGGCAGCC CGGCCAGGG CAACTACGCG	30360
	GCGGCCAACG CCACCTCGA CGCCCTCGCC GCCCGCGCC GGTCCCTCGG CCTCCCGTCG	30420
	GTGTCACTCG CCTGGGGTCT GTGGTCCGAC ACCAGCCGA TGGCACACGC ACTGGACCAG	30480
10	GAGAGCCTCC AGCGGCGCTT CGCCCGCAGC GGCCTCCCGC CCCTGTCCGC CACGCTGGGC	30540
	GCCGCGCTGT TCGACGCCGC CCTGCGGGTC GACGAGCCG TGCAGGTCCC CATGCGGTTC	30600
	GACCCGGCCG CGCTGCGCGC CACCGGAAGC GTCCCGCCC TGCTGTGCGA CCTGTCGGG	30660
15	TCCGCCCCGG CGACCGGGTC CGCGCCCCG GCGTCCGGC CCCTTCCGGC TCCGGACGCC	30720
	GGGACGTCG GCGAGCCGCT CGCCGAGCGG TTGGCCGGAC TCTCCGCCGA GGAACGCCAC	30780
	GACCGGCTGC TCGGCCTGGT CGGCGAACAC GTGGCCGGG TACTGGGCCA CGGCTCCGCC	30840
20	GCCGAGGTCC GGCCCGACCG GCCGTTCCGC GAGGTGGGT TCGACTCGCT CACGGCCGTG	30900
	GAACTGCGCA ACCGGATGGC GCGGTACAC GGGGTACGG TCCCGCCAC CCTGGTCTTC	30960
25	GACCACCCCA CCCCCGCCGC GCTGTCTCG CACCTCGACG GCCTGCTGGC CCCGGCACAG	31020
	CCGTCACCA CCACACCGCT GCTGTCCGAA CTGGACCGCA TCGAGGAGGC CCTGGCCGCC	31080
	CTACCCCCG AGCACCTCGC GGAGCTCGC CCCGCCCCG ACGACCGGC CGAGGTGCGC	31140
30	CTGCGCCTGG ACGCCCTGGC CGACCGCTGG CGCGCCCTGC ACGACGGCGC GCCCGGCGCC	31200
	GACGACGACA TCACCGACGT GCTGAGCAGC GCCGACGAC ACGAGATCTT CGCGTTCATC	31260
	GACGAGCGGT ACGGCACGTC GTGACCGCC GCCCGAGCC CCGCCCGTCA TCGAAAGGAA	31320
35	GCACCACCAT GGCGAACGAA GAGAAGCTGC GCGCTACCT CAAGCGGTG ACGGGTGAGC	31380
	TGCACCGGGC CACCGAGCAG CTGCGTGCCC TGGACCGGC GGCCACGAG CCGATCGCGA	31440
40	TCGTGCGGGC GGCCTGCCGA CTCCCCGGC GCGTCGAGAG TCCGGACGAC CTGTGGGAGC	31500
	TGCTGCACGC CGGTGCCGAC GCGGTCCGCC CGGCCCCGC CGACCGCGC TGGGACGTGG	31560
	AGGGAAGGTA CTGCCCCGAC CCCGACACG CCGCACCTC GTACTGCCG GAGGGCGGCT	31620
45	TCGTGCAGGG GGCCGACCGG TTCGACCCG CCCTCTTCGG CATCTCGCCC AACGAGGCGC	31680
	TCACCATGGA CCCCCAGCAG CGGCTGCTGC TGGAGACCTC CTGGGAGGCG CTGGAGCGAG	31740
	CCGGTCTGGA CCCCCAGTCC CTGGCGGGCA GCCCGACCG CGTGTTCCGC GGGGCGTGGG	31800
50	AGAGCGGCTA CCAGAAGGGC GTCGAAGGGC TCGAAGCCGA TCTGGAGGCC CAACTCCTCG	31860
	CCGGCATCGT CAGCTTCACC GCCGCGCGC TCGCTACGC CCTGGGCTTG GAGGGCCCCG	31920
	CGCTGACGAT CGACACGGCC TGCTCCTCGT CGTGGTGGC ACTGCACCTG GCGGTGCACT	31980
55	CACTGCGCCG GGGCGAGTGC GACCTCGCAC TGGCGGGCG CGCCACGGTC ATCGCCGACT	32040

EP 0 791 655 A2

	TCGCGCTCTT	CACCCAGTTC	TCCCGGCAGC	GCGGGCTCGC	CCCCGACGGG	CGGTGCAAGG	32100
5	CCTTCGGTGA	GACGCGCGAC	GGCTTCGGCC	CCGCCGAGGG	CGCGGGGATG	CTGCTGGTCG	32160
	AGCGGTGTC	GGACGCCCCG	CGCAACGGGC	ACCCGGTGCT	GGCGGTGGTG	CGGGGCAGTG	32220
	CCGTCAACCA	GGACGGTGCG	AGCAATGGGC	TGACGGCGCC	GAGTGGTCCT	GCGCAGCAGC	32280
10	GGGTGATCCG	TGAGGCGCTG	GCCGACGCGG	GGCTGACGCC	CGCCGACGTG	GACGCGGTG	32340
	AGGCGCACGG	CACCGGCACG	CCGCTCGGCG	ACCCCATCGA	GGCCGGCGCG	CTCATGGCGA	32400
	CGTACGGGCA	CGAACGGACG	GCGACCCCGC	TGTGGCTGGG	TTCGCTGAAG	TCGAACATCG	32460
15	GGCACACCCA	GGCCGCCGCC	GGCGTGGCCG	GGGTGATCAA	GATGGTGCTG	GCGCTGCGCC	32520
	ACGGTGAGCT	GCCCGGCACC	CTGCACGCGT	CGACGGCGTC	CTCCAGGATC	GAATGGGACG	32580
	CGGGCGCCGT	GGAGTTGCTG	GACGAGGCCA	GGCCCTGGCC	CCGGCGTGCC	GAGGGGCCGC	32640
20	GCCGGGCGGG	CATCTCCTCG	TTCGGCATCA	GCGGCACCAA	CGCGCACCTC	GTCATCGAGG	32700
	AGGAGCGCC	CGCCCGGCCG	GAGCCCGAGG	AGGCCCGCGA	GCCGCCCGCC	CCGGCCACCA	32760
25	CCGTCTCCC	GCTGTCGGCC	GCCGGCGCGC	GATCCCTGCG	CGAGCAGGCC	CGCAGGCTCG	32820
	CCGCGCACCT	GGCCGGCCAC	GAGGAGATCA	CCGCCGCCGA	CGCCGCCCGC	TCCGCCGCCA	32880
	CCACCGTGC	CGCGCTCTCG	CACCGGGCCT	CGGTCTTGCC	CGACGACCGG	CGGGCGCTGA	32940
30	TCGACAGGCT	GACCGCGCTG	GCGGAGGACA	GGAAGGACCC	CGGCGTCACC	GTCGGCGAGG	33000
	CGGGCAGCGG	CGGCCCCCCC	GTCTTCGTCT	TCCCGGGACA	GGGCTCCCAG	TGGACGGGCA	33060
	TGGGCGCCGA	ACTCCTGGAC	AGGGCACCAG	TCTTCCGCGC	CAAGGCCGAG	GAGTGGCGGC	33120
35	GGGCCCTCGC	GGCCACCTC	GA CTGGTCGG	TGCTCGACGT	CCTGCGCGAC	GCGCCCGGCG	33180
	CCCCGCCGAT	CGACCGCGCG	GACGTCGTCC	AGCCGACCCT	GTTCAACATG	ATGGTCTCCC	33240
40	TCGCGGCGCT	GTGGGAGTCC	CACGGTGTAC	GGCCCGCGCG	CGTGGTCGGC	CACTCCCAAG	33300
	GCGAGATCGC	CGCCGCCAC	GCGGCCGGTG	CCCTGTCCCT	CGACGACGCG	GCCCGCGTGA	33360
	TCGCCGAGCG	CAGCAGGCTC	TGGAAGCGCG	TGGCCGGAAA	CGGCGGCATG	CTCTCCGTGA	33420
45	TGGCCCCGGC	CGACCGGGTC	CGCGAACTGA	TGGAGCCCTG	GGCGGAGCGG	ATGTCCGTGG	33480
	CCGCCGTCAA	CGCCCCCGCC	TCGGTCACCG	TGGCCGGTGA	CGCGCGGGCG	CTGGAGGAGT	33540
	TCGGCGGCCG	GCTCTCCGCC	GCCGGGTGCG	TGCGCTGGCC	CCTCGCCGGC	GTCGACTTCG	33600
50	CCGGACACTC	ACCCAGGTG	GAGCAGTTCC	GCGCCGAGCT	CCTCGACACG	CTGGGCACCG	33660
	TCCGCCCGAC	CGCCGCCCGG	CTGCCCTTCT	TCTCCACCGT	GACCGCCGCG	GCGCACGAGC	33720
	CCGAAGGCCCT	GGACGCCGCG	TACTGGTACC	GGAACATGCG	CGAACCCGTG	GAGTTCGCGT	33780
55	CCACCCTGCG	GACGCTGCTG	CGCGAGGGCC	ACCGCACCTT	CGTCGAGATG	GGCCCGCACC	33840

EP 0 791 655 A2

	CCCTGCTGGG CGCCGCGATC GACGAGGTCG CCGAGGCCGA GGGCGTGCAC GCCACCGCCC	33900
5	TGCCCACCCT CCACCGCGGC TCCGGCGGCC TGGACCGGTT CCGCTCCTCG GTGGGCGCCG	33960
	CGTTCCGCCA CGGAGTACGG GTCGACTGGG ACGCCCTCTT CGAGGGCTCC GCGCCCCGCC	34020
	GGGTCCCGCT GCCACCTAC GCCTTCAGCC GGGACCGGTA CTGGCTGCCC ACCGCCATCG	34080
10	GCCGGCGCGC CGTCGAGGCG GCCCCGTCG ACGCGTCCGC CCCCAGGCGC TACCGCGTCA	34140
	CCTGGACACC CGTGGCATCC GACGACTCCG GCCGCGCCTC CCGGCGCTGG CTGCTGGTGC	34200
	AGACCCCCCG CACCGCGCCG GACGAGGCGG ACACCGCGGC GTCCGCCCTC GGTGCGGCCG	34260
15	GGGTGGTCGT GGAGCGCTGC CTGCTGGATC CCACCGAGGC CGCGCGCGTC ACGCTCACC	34320
	AGCGACTGGC CGAACTGGAC GCGCAGCCGG AGGGCCTGGC CGGCGTGTG GTGCTGCCCC	34380
	GCCGTCCGCA GAGCACCACA CCGCCGACG CCTCCCCGCT CGACCCGGGG ACGGCCGCCG	34440
20	TCCTGCTCGT GGTCCAGGCC GTGCCGACG CCGCTCCGAA GGCCCGGATC TGGGTGGTGA	34500
	CGCGGGGTGC GGTGGCGGTG GGTGCGGTG AGGTGCCGTG TGCGGTGGGT GCGCGGTGT	34560
25	GGGGTCTGGG GCGGGTGGCT GCGTTGGAGG TGCCGGTGCA GTGGGGTGGG TTGGTGGATG	34620
	TGGCGGTGGG GCGGGTGTG CTGAGTGGC GTCGTGTGTT GGGTGTGTT GCGGGGGTGC	34680
	GTGAGGATCA GGTGCGGTG CGTGGTGGG GTGTGTTCCG TCGTCGTCTG GTGGGTGTGG	34740
30	GGGTCCGGG TGTTCCGGG GTGTGGCGTG CCGCGGGGTG TGTGTTGTT ACCGGTGGGT	34800
	TGGGTGGTGT GGGGGTTCAT GTGGCGCGGT GGTGGCGCG TTCCGGTGCG GAGCATGTGG	34860
	TGTTGCCGGG GCGTCGGGT GGTGGGGTTG TGGGGCGGT GGAGTTGGAG CCGGAGTTGG	34920
35	TGGGGTTGGG GGCGAAGGTG ACGTTCGTTT CGTGTGATGT GGGGATCGG GCGTCGATGG	34980
	TGGGGTTGTT GGTGTGTTG GAGGGGTGG GGTGCGGTT GCGTGGTGTG TTTCATGCGG	35040
	CGGGGGTGGC TCAGGTGTG GGGTTGGGTG AGGTGTGTT GGCGGAGGCG GGTGGTGTGT	35100
40	TGGGGGTAA GCGGTGGGG GCTGAGTTGT TGGACGATT GACGGCGGGT GTGGAGCTGG	35160
	ATCGTTCTGT GTTGTCTCG TCGGTCCTG GGTGTGGGG GAGTGGGGG CACTCGGTGT	35220
45	ATCGGCGGC CAATGCGCAT CTGGATGCGT TGGCGGAGCG TCGTCGTGCG CAGGGCGTC	35280
	CCGCGACCTC CGTCGCCTGG GGCCTGTGGG GCGCGAGGG CATGGGAGCG GACGAAGGCG	35340
	TCACGGAGTT CTACGCCGAG CGCGGCCTCG CCCCCATCG GCCCGAGTCG GGCATCGAGG	35400
50	CACTGCACAC GGCCTGAAC GAGGGCGACA CCTGCGTCAC GGTGCGCGAC ATCGACTGGG	35460
	AACACTTCGT CACCGGGTTC ACCGCCTACC GGCCAGCCC GCTGATCTCC GACATCCCCC	35520
	AGGTCCGCGC GTTGGCACG CCCGAACCCA CCGTGGACGC CTCGGACGGA CTGCGCCGGC	35580
55	GCGTCGACGC CGCCCTCACC CCGCGCGAGC GCACCAAGGT CCTGGTCGAC CTGGTCCGCA	35640

EP 0 791 655 A2

	CGGTGGCGGC	GGAGGTCCTC	GGTCACGACG	GGATCGGCGG	CATCGGCCAC	GACGTGGCCT	35700
5	TCCGGGACCT	CGGCTTCGAC	TGGCTGGCCG	CGGTCCGGAT	GCGCGGCCGG	CTGGCCGAGG	35760
	CGACCGGACT	CGTACTGCCC	GCGACGGTCA	TCTTCGACCA	CCCCACCGTG	GACCGGCTCG	35820
	GCGGCGCGCT	GCTGGAGCGG	CTGTCCGCGG	ACGAACCCGC	GCCCGGCGGG	GCGCCGGAGC	35880
10	CCGCCGGGGG	GAGGCCCGCG	ACCCACCGC	CCGCACCGGA	GCCGGCCGTC	CACGACGCCG	35940
	ACATCGACGA	ACTCGACGCG	GACGCCCTGA	TCCGGCTGGC	CACGGGAACC	GCCGGACCGG	36000
	CCGACGGCAC	GCCGGCCGAC	GGCGGGCCCG	ACGCGCGGGC	GACCGCCCCC	GACGGAGCAC	36060
15	CGGAGCAGTA	GCGCGCCCTC	ACCGGCGCGC	CGACCGGCGG	AGCGCCGTAC	CGCCGACGCC	36120
	CCCCACAGCC	AGCGAGCAGA	CGAGGAAGCC	GAAGATGTCA	CCGTCCATGG	ACGAAGTGCT	36180
	GGGTGCGCTG	CGCACCTCCG	TCAAGGAGAC	CGAGCGGCTG	CGCCGGCACA	ACCGGGAGCT	36240
20	CCTGGCCGGC	GCGCACGAGC	CGGTCCGCAT	CGTGGGCATG	GCCTGCCGCT	ACCCCGGTGG	36300
	CGTGAGCACC	CCGGACGACC	TGTGGGAGCT	CGCCGCGGAC	GGCGTCGACG	CGATCACCCC	36360
25	CTTCCCGGCC	GACCGGGGCT	GGGACGAGGA	CGCCGTCTAC	TCGCCCAGAC	CCGACACCCC	36420
	CGGCACCACC	TACTGCCGTG	AGGGCGGCTT	CCTCACCGGC	GCCGGGGACT	TCGACGCGGC	36480
	CTTCTTCGGC	ATCTCGCCGA	ACGAGGCGCT	GGTGATGGAC	CCGCAGCAGC	GGCTGTTGCT	36540
30	GGAGACGTCG	TGGGAGACGT	TGGAGCGGGC	CGGCATCGTC	CCCGCGTCGC	TGCGCGGCAG	36600
	CCGTACCGGT	GTCTTCGTCG	GAGCCGCGCA	CACGGGATAC	GTCACCGACA	CCGCGCGAGC	36660
	GCCCCAGGGC	ACCGAGGGCT	ATCTGCTGAC	GGGCAACGCC	GATGCCGTCA	TGTCCGGCCG	36720
35	GATCGCCTAC	TCCCTGGGTC	TGGAGGGGCC	GGCGCTGACG	ATCGGGACGG	CCTGCTCGTC	36780
	GTCGTTGGTG	GCGTTGCATC	TGGCGGTGCA	GTCGTTGCGG	CGGGGCGAGT	GCGACCTGGC	36840
40	GTGCGCCGGC	GGCGTCGCGG	TCATGCCCGA	CCCGACGGTG	TTCGTGGAGT	TCTCGCGGCA	36900
	GCGGGGGCTG	GCGGTGGACG	GGCGGTGCAA	GGCGTTCGCG	GAGGGTGGCG	ACGGGACGGC	36960
	GTGGGCGGAG	GGAGTGGGTG	TGCTGCTGGT	GGAGCGGCTT	TCCGACGCGC	GCCGCAATGG	37020
45	CCATCGGGTG	CTGGCGGTGG	TGCGGGGCAG	TGCGGTCAAT	CAGGACGGGG	CGAGCAATGG	37080
	GCTGACGGCG	CCGAGTGGTC	CTGCGCAGCA	GCGGGTGATC	CGTGAGGCGC	TGGCTGATGC	37140
	GGGGCTGACG	CCCGCCGACG	TGGATGTGGT	GGAGGCGCAC	GGTACGGGGA	CGGCGTTGGG	37200
50	TGATCCGATC	GAGGCGGGTG	CGTTGCTGGC	CACGTACGGG	CGGGAGCGGG	TCGGTGATCC	37260
	TTTGTGGTTG	GGGTCTGTGA	AGTCGAACAT	CGGGCATGCG	CAGGCGGCTG	CGGCTGTGGG	37320
	TGGTGTGATC	AAGGTGGTGC	AGGCGATGCG	GCATGGGTGC	TTGCCGCGGA	CGCTGCATGT	37380
55	GGATGCGCCG	TCGTGGAAGG	TGGAGTGGGC	TTCGGGTGCG	GTGGAGCTGC	TGACCGAGGG	37440

EP 0 791 655 A2

	CCGGTCGTGG	CCGCGGCGGG	TGGAGCGGGT	GCGGCGGGCC	GCGGTGTCGG	CGTTCGGGGT	37500
5	GAGCGGGACC	AACGCCCCATG	TGGTCCTCGA	GGAAGCACCG	GTCGAGGCCG	GGAGCGAGCA	37560
	CGGGGACGGC	CCCGGACCCG	ACCGGCCCCGA	CGCGGTGACG	GGTCCGCTCC	CCTGGGTGCT	37620
	CTCGGCACGC	TCGCGGGAGG	CGCTGCGCGG	CCAGGCCGGA	CGACTCGCCG	CTCTCGCCCC	37680
10	CCAGGGGCGC	ACGGAGGGCA	CCGGCGGCGG	CAGCGGACTC	GTCGTCCCCG	CGGCCGACAT	37740
	CGGATACTCC	CTGGCCACCA	CCAGGAGAC	CCTGGAGCAC	CGGGCGGTGG	CGCTGGTGCA	37800
	GGAGAACCGG	ACGGCCGGGG	AGGACCTCGC	CGCGCTGGCC	GCCGGCCGCA	CACCGGAGAG	37860
15	CGTGGTCACG	GGTGTGCGGC	GACGTGGCCG	CGGGATCGCC	TTCTCTTGCT	CGGGGCAGGG	37920
	CGCCCAGCGG	CTCGGCGCCG	GTCGGGAGCT	CCGCGGCAGG	TTCCCCGTCT	TCGCCGACGC	37980
	CCTCGACGAG	ATCGCGGCGG	AGTTGACGCG	CCACCTCGAA	CGCCCTCTCC	TGTCGGTGAT	38040
20	GTTCCGCCGAG	CCCGCCACGC	CGGACCCCGC	ACTCCTCGAC	CGCACCGACT	ACACCCAGCC	38100
	GGCCCTCTTC	GCGGTGGAGA	CCGCGCTCTT	CCGGCTCCTG	GAGAGCTGGG	GCCTGGTCCC	38160
25	GGACGTCTTC	GTGGGCCACT	CGATCGGCGG	TCTGGTGGCG	GCTCACGTGG	CGGGCGTCTT	38220
	CTCTGCGGCC	GACGCGGCCC	GGCTGGTCTC	CGCACGCGGC	CGGCTCATGC	GGGCCCTGCC	38280
	CGAGGGCGGC	GCGATGGCGG	CCGTGCAGGC	CACCGAGCGG	GAGGCCGCGG	CGCTGGAGCC	38340
30	CGTCGCCGCC	GCGGCGCGGG	TGGTCGCGGC	GGTCAACGGC	CCGCAGGCCC	TCGTGCTCTC	38400
	CGGGGACGAG	GCGGCCGTAC	TGGCGGCGGC	CGGTGAAGTG	GCCGCCCGCG	GACGCCGCAC	38460
	CAAGCGCCTG	AGGGTGAGCC	ACGCCTTCCA	CTACCCCCGT	ATGGACGCCA	TGCTCGCCGA	38520
35	CTTCCGCGCG	GTGGCGGACA	CGGTGACTA	CCACGCCCCC	CGGCTGCCGG	TCGTCTCCGA	38580
	AGTGACCGGC	GACCTCGCCG	ACGCCGCCCA	GCTGACCGAC	CCCGGCTACT	GGACCCGCCA	38640
	GGTGCGGCAG	CCGGTGCCT	TCGCCGACGC	CGTGCGCACC	GCGAGCGCCC	GGGACGCCGC	38700
40	GACCTTCATC	GAGCTCGGGC	CCGACCCCGT	CCTGTGCGGC	ATGGCGGAGG	AGTCCCTGGC	38760
	CGCGGAGGCC	GACGTGCTGT	TCGCCCCGGC	ACTGCGCCGC	GGGCGCCCGG	AGGGCGACAC	38820
45	CGTGCTCCGG	GCCGCCGCGA	GCGCGTACGT	CCGCGGCGCG	GGCCTCGACT	GGGCCGCGCT	38880
	CTACGGCGGC	ACGGGAGCCC	GCCGCACCGA	CCTGCCACCC	TACGCCTTCC	AGCACAGCCG	38940
	CTACTGGCTC	GCCCCCGCCT	CGGCCCGGGT	CGCCCCCGCG	ACGGCCGCCC	CCTCCGTCCG	39000
50	ATCCGTGCCG	GAAGCCGAGC	AGGACGGGGC	GCTGTGGGCC	GCCGTGCACG	CCGGTGACGT	39060
	CGCCTCGGCC	GCGGCGCGAC	TGGGCGCCGA	CGACGCCGGT	ATCGAACACG	AACTGCGCGC	39120
	GGTCCTGCCG	CACCTGGCCG	CCTGGCACGA	CCGCGACCGC	GCGACCGCGC	GGACCGCGGG	39180
55	CCTGCACTAC	CGCGTCACCT	GGCAGGCGAT	CGAGGCAGAC	GCTGTCAGGT	TCAGCCCCCTC	39240

EP 0 791 655 A2

	GGATCGCTGG CTGATGGTCG AGCATGGGCA GCACACGGAA TGC CGCGACG CCGCGGAACG	39300
5	GGCGCTGCGC GCGGCCGGCG CGGAGGTCAC CCGCCTGGTG TGGCCGCTGG ACCAGCACAC	39360
	CGGATCACCG CGGACGGAGA CCCCCGACCG CGGCACCCTG GCGGCCCGGC TGGCCGAGCT	39420
	CGCACGGAGC CCGGAGGGCC TGGCCGGCGT GCTGCTGCTC CCGGACTCGG GCGGTGCCGC	39480
10	GGTCGCCGGG CACCCCGGGC TGGACCAGGG AACGGCGGGC GTGCTGCTGA CGATCCAGGC	39540
	ACTGACCGAC GCCCGGGTGC GGGCACCGCT GTGGGTGGTG ACCCGGGGTG CCGTGGCGGT	39600
	GGGTTCGGGT GAGGTGCCGT GTGCGGTGGG TGC CGGGTG TGGGTCTGG GCGCGGTGGC	39660
15	TGCGTTGGAG GTGCCGGTGC AGTGGGGTGG GTTGGTGGAT GTGGCGGTGG GGGCGGGTGT	39720
	GCGTGAGTGG CGTCGTGTGG TGGGTGTGGT TGGCGGGGGT GGTGAGGATC AGGTGGCGGT	39780
	GCGTCCTCGC GGTGTGTTCG GTCGTCGTCT GGTGGGTGTG GGGGTGCGCG GTGGTTCCGG	39840
20	GGTGTGGCGT GCGCGGGGGT GTGTGGTGGT GACGGGTGGG TTGGGTGGTG TGGGGGGTCA	39900
	TGTGGCGCGG TGGTTGGCGC GTTCCGGTGC GGAGCATGTG GTGTTGGCGG GCGCTCGGGG	39960
25	TGGTGGGGTT GTGGGGGCGG TGGAGTTGGA GCGGGAGTTG GTGGGGTTGG GGGCGAAGGT	40020
	GACGTTCTGT TCGTGTGATG TGGGGGATCG GCGCTCGGTG GTGGGGTTGT TGGGTGTGGT	40080
	GGAGGGGTG GGGGTGCCGT TCGGTGGTGT GTTTCATGCG GCGGGGGTGG CTCAGGTGTC	40140
30	GGGGTTGGGT GAGGTGTCTG TGGCGGAGGC GGGTGGTGTG TTGGGGGGTA AGGCGGTGGG	40200
	GGCTGAGTTG TTGGACGAGT TGACGCGGGG TGTGGAGCTG GATGCGTTCC TGTGTGTTCTC	40260
	GTCGGGTGCT GGGGTGTGGG GGAGTGGGGG GCAGTCGGTG TATGCGGCGG CCAATGCGCA	40320
35	TCTGGATGCG TTGGCGGAGC GTCGTCTGTC GCAGGGGCGT CCGCGACCT CCGTCGCCTG	40380
	GGGCCCGTGG GACGGCGACG GCATGGGCGA GATGGCGCCC GAGGGCTACT TCGCCCGCCA	40440
40	CGGCGTGGCC CCGCTCCACC CCGAGACGGC GCTCACCGCC CTGCACCAGG CCATCGACGG	40500
	CGGCGAAGCC ACGGTCACCG TGGCGGACAT CGACTGGGAA CGGTTCGCCC CCGGCTTCAC	40560
	CGCCTTCGCT CCCAGCCCCC TGATCGCCGG CATCCCCCGG GCGCGTACGG CGCCCGCCGC	40620
45	CGGCCGGCCC GCCGAGGACA CCCCCACCGC CCGCGGCTC CTGCGGGCGC GGCCCGAGGA	40680
	CCGGCCGCGG CTCGCCCTGG ACCTGGTGCT CCGCCACGTC GCGGCGGTCC TCGGCCACTC	40740
	CGAGGACGCC CGGGTGACG CCCGGGCCCC CTTCGGGGAC CTCGGCTTCG ACTCGCTCGC	40800
50	CGCGGTGCGG CTGCGCCGCC GGCTGGCCGA GGACACCGGG CTCGACCTGC CCGGCACCCT	40860
	CGTCTTCGAC CACGAGGACC CCACCGCGCT GGGCCACCAC CTGGCCGGCC TCGCCGACGC	40920
	GGGGACCCCC GGCCCCCAGG AGGGCACGGC TCGGGCCGAG AGCGGGCTGT TCGCCTCCTT	40980
55	CCGCGCCGCC GTCGAACAGC GCAGGTGAG CGAGGTGCTG GAGCTGATGG CCGACCTGGC	41040

EP 0 791 655 A2

	GGCGTTCCGG CCGCCTACT CCCGGCAGCA CCCC GGCTCC GGCCGCCCCG CGCCCGTACC	41100
5	CCTCGCGACC GGACCGGCGA CGCGTCCCAC GCTGTACTGC TCGCCCGGCA CCGCGGTCCG	41160
	CTCCGGGCCC GCCGAGTACG TCCCGTTCGC CGAAGGACTG CGCGCGCTCC GGGAGACGGT	41220
	CGCCCTTCCC CTGTCCGGCT TCGGCAGCCC CGCGGAACCG ATGCCCCGAT CGCTCGACGC	41280
10	GCTGATCGAG GTCCAGGCCG ACCTCCTCCT GGAGCACACC GCGGGCAAGC CCTTCGCCCT	41340
	CGCCGGCCAC TCCGCCGGCG CGAACATCGC CCACGCCCTG GCCGCCCGGC TGGAGGAACG	41400
	CGGCTCGGGC CCCGCAGCCG TCGTACTGAT GGACGTCTAC CGTCCCGAGG ACCCCGGTGC	41460
15	GATGGGCGAG TGGCGCGACG ACCTGCTCAG CTGGGCGCTC GAACGCAGCA CCGTGCCCTT	41520
	GGAGGACCAC CGGCTCACCG CCATGGCCGG CTATCAGCGG CTGGTGCTCG GAACCCGGCT	41580
	CACCGCCCTC GAAGCCCCCG TCCTGCTGGC CCGGGCGTCC GAACCCCTGT GCGCGTGGCC	41640
20	GCCCGCGGGC GGGGCGCGGG GCGACTGGCG GTCCCAGGTC CCGTTCGCAC GGACCGTCGC	41700
	CGACGTGCCC GGCAACCACT TCACCATGCT CACCGAACAC GCCCGGCACA CCGCGTCCCT	41760
25	GGTGACGAA TGGCTGGACA GCCTCCCGCA CCAGCCCGGT CCGCCCCGC TCACCGGAGG	41820
	GAAACACTGA TGTACGCGA CGACATCGCG GCCGTCTACG ACCTGGTCCA CGAGGGGAAG	41880
	GGGAAGGACT ACCGGCAGGA GGCCGAGGAG ATCGCCGCAC TCGTGCGCGT CCACCGGCCG	41940
30	GGCGCCCGGA CCTTGCTCGA CGTGGCCTGC GGCACCGGCC AGCACCTGCA CCACCTGGAC	42000
	GGCTCTTCG ACCACGTGCA GGGCCTGGAA CTCTCCGCGC ACATGTGGC CTTCCGAC	42060
	GGCCGGAACC CCGGTGTCAC CTTCCACCAA GGGGACATGC GCTCGTTCTC CTTGGGACGC	42120
35	CGGTTGACG CGGTGACCTG CATGTTTACG TCCATAGGCC ACCTGCGGAC CACCGACGAA	42180
	CTCGACAGCA CGGTGCGGGC CTTACCGAC CACCTCGAAC CGTCCGGCGT CATCGTCTC	42240
	GAACCCTGGT GGTTCCTCGA GTCTTTCACC CCGGTTACG TCGGCGCCAG CATCAGGAG	42300
40	GCGGGCGAGC GCACCGTCTG CCGGGTCTCG CACTCCGTAC GGGAGGGGAA CGCCACCCGC	42360
	ATCGAGGTGC ACTACCTCCT CGCCGGACCC GGCGGCGTCC GTCACCTGAC CGAGGACCAC	42420
45	ACCATCACCC TGTTCCTCGG CGCCGACTAC GAGGCGGCCT TCGAGCGCGC CGGCTGCGAC	42480
	GTGGTCTACC AGGAAGGCGG CCCGTCCGGT CGCGGGCTGT TCATCGGCAC CCGCGCTGA	42540
	CCCGGTGCGG ACGCGGACCG CCGCGGCCCG GAGGCGGGTT GCGCCGACCC ACCCGGCACA	42600
50	CCCGGTCCC CCGATCGTGC GAGCGCCCCC ATCGACCCGA GAAGAAAGGC AGGGCAGCCA	42660
	TGCCCCACCT TGCCACGGAA ACGGCCCCCG CGAGCACGAG CACGAGCGCG GGCACGAGCA	42720
	CGGGCGTCCG TCGGCTCGGC CGTCGGCTCC AGCTGACCCG GGCCGCACAC TGGTGCGCCG	42780
55	GCAACCAGGG CGACCCGTAC GCGCTGATCC TGCGCGCCGT CGCCGACCCG GAGCCGTTCG	42840

AACGGGAGAT CCGGGCCCGC GGACCGTGGT TCCGCAGCGA ACAGCTGGAC GCCTGGGTGA 42900
 5 CCGCGGACCC CGAGGTGGCG GCGGCCGTCC TGGCCGACCC GCGCTTCGGC ACGCTGGACC 42960
 GGGCCGACG CCGCCCGGAC GAGGAACTGC TGCCCTCGC CGAGGCGTTC CCCCACCACG 43020
 AACGCGCGGA GCTCGTACGC CTGCGGGCGC TGGCCGCCCC GGTGCTCAGC CGGTACGCCC 43080
 10 CGGCCCAGGC GCCCTGCGCG GCGCGCACCA CCGCCCGCAG AGTGCTCGGC CGCCTGCTGC 43140
 CCACCGGTGA CGCCGGGTTC GACCTTGTCG GCGAGTTCG CCGGCCCTAC GCCGTGAGC 43200
 TGATGCTCAG GTCCTCGGA GTGCCGGGCC GCGACCGCGC CACCGCCGCG CGGGCACTCG 43260
 15 CCGCTGCGG CCCCCAGCTC GACGCCCGGA TGGCCCCGCA ACTGCTGACC GTGGCCCCGG 43320
 AGTCGCGCA CGCCGTCCG AACTGGCCG ACCTGGTCCC CGAGCTCGTC GCGGAGAAGT 43380
 CCGGGGGCCT CGGAACGCC GAGCCCCGCG CCGACGACGT GCTCGCCCTC CTCTGCACG 43440
 20 ACGGCGTCG CCGCGGCGAC GTCGAGCGCA TCGCGCTGCT CCTGCGGTTC GGCGCACCCG 43500
 AACCCTGCT CACCGCCGTC GCGCACACGG TCCACCGGT GCTCGGCCGG CCGGGGGAGT 43560
 GGGAGAGGGC CCGCCGGACG CCGGCCGCGG CGAACGCCGT CGACCAGGTG CTGCGCGAGC 43620
 25 GCCCCCGGC CCGCTGGAG AACCGGGTCG CGCACACCGG CCTCGAACTC GGCGGCCGCC 43680
 GGATCACCGC CGACGAGCAC GTCGTGGTGC TGGCCGCGC CGGACGGAG ATCCCCGGGC 43740
 CGGAGCCGCT CCGGGGCGCC GACGGACCGC ACCTGGCGCT CGCCCTCCCG CTGATCCGCC 43800
 TGGCCGCCAC CACCGCGGTC CAGGTACGG CCGGCCGCT CCGCGGCTG CCGGCCGAGG 43860
 GACCGCCCCT GACCGGGCCG CGGTACCGG TCCTGGGCGC CTGCGCCCGC CTCCGGGTCC 43920
 30 ACCCGGGATG ACCCGCCGT CCGTACGCCC CCTCCCAGAC CGGAGCCGCT GTGCGCGTCC 43980
 TGCTGACATC CCTCGCCAC AACACCCACT ACTACAGTCT GGTGCCCCCTC GCCTGGGCGC 44040
 TGGCGCGCGC CCGGCACGAG GTACGGGTGG CGAGCCCGCC CTCCCTCACC GACGTCATCA 44100
 40 CCTCCACCG TCTGACCGC GTACCGGTGG GCGACGACG ACCGGCCGCG GAGCTGCTCG 44160
 CCGAGATGG CAGAGACCTC GTCCCTACC AGAGGGGCTT CGAGTTCGGT GAGGTGGAGA 44220
 45 3GCGAGGAGGA GACCACCTGG GAGTACCTGC TGGCCAGCA GAGCATGATG GCCGCCCTGT 44280
 GCTTCGCCCC GTTCAACGGC GCCGCCACGA TGGACGAGAT CGTCGACTTC GCCCGTGGCT 44340
 GGCGGCCCGA CCTGGTCTGT TGGGAACCCT GGACCTA 44377

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4550 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

5 Met Ser Gly Glu Leu Ala Ile Ser Arg Ser Asp Asp Arg Ser Asp Ala
 1 5 10 15
 10 Val Ala Val Val Gly Met Ala Cys Arg Phe Pro Gly Ala Pro Gly Ile
 20 25 30
 Ala Glu Phe Trp Lys Leu Leu Thr Asp Gly Arg Asp Ala Ile Gly Arg
 35 40 45
 15 Asp Ala Asp Gly Arg Arg Arg Gly Met Ile Glu Ala Pro Gly Asp Phe
 50 55 60
 Asp Ala Ala Phe Phe Gly Met Ser Pro Arg Glu Ala Ala Glu Thr Asp
 65 70 75 80
 20 Pro Gln Gln Arg Leu Met Leu Glu Leu Gly Trp Glu Ala Leu Glu Asp
 85 90 95
 Ala Gly Ile Val Pro Gly Ser Leu Arg Gly Glu Ala Val Gly Val Phe
 100 105 110
 25 Val Gly Ala Met His Asp Asp Tyr Ala Thr Leu Leu His Arg Ala Gly
 115 120 125
 Ala Pro Val Gly Pro His Thr Ala Thr Gly Leu Gln Arg Ala Met Leu
 130 135 140
 30 Ala Asn Arg Leu Ser Tyr Val Leu Gly Thr Arg Gly Pro Ser Leu Ala
 145 150 155 160
 Val Asp Thr Ala Gln Ser Ser Ser Leu Val Ala Val Ala Leu Ala Val
 165 170 175
 35 Glu Ser Leu Arg Ala Gly Thr Ser Arg Val Ala Val Ala Gly Gly Val
 180 185 190
 Asn Leu Val Leu Ala Asp Glu Gly Thr Ala Ala Met Glu Arg Leu Gly
 195 200 205
 40 Ala Leu Ser Pro Asp Gly Arg Cys His Thr Phe Asp Ala Arg Ala Asn
 210 215 220
 Gly Tyr Val Arg Gly Glu Gly Gly Ala Ala Val Val Leu Lys Pro Leu
 225 230 235 240
 45 Ala Asp Ala Leu Ala Asp Gly Asp Pro Val Tyr Cys Val Val Arg Gly
 245 250 255
 50 Val Ala Val Gly Asn Asp Gly Gly Gly Pro Gly Leu Thr Ala Pro Asp
 260 265 270
 Arg Glu Gly Gln Glu Ala Val Leu Arg Ala Ala Cys Ala Gln Ala Arg
 275 280 285
 55 Val Asp Pro Ala Glu Val Arg Phe Val Glu Leu His Gly Thr Gly Thr

EP 0 791 655 A2

	290		295		300
5	Pro Val Gly Asp Pro Val Glu Ala His Ala Leu Gly Ala Val His Gly 305 310 315 320				
	Ser Gly Arg Pro Ala Asp Asp Pro Leu Leu Val Gly Ser Val Lys Thr 325 330 335				
10	Asn Ile Gly His Leu Glu Gly Ala Ala Gly Ile Ala Gly Leu Val Lys 340 345 350				
	Ala Ala Leu Cys Leu Arg Glu Arg Thr Leu Pro Gly Ser Leu Asn Phe 355 360 365				
15	Ala Thr Pro Ser Pro Ala Ile Pro Leu Asp Gln Leu Arg Leu Lys Val 370 375 380				
	Gln Thr Ala Ala Ala Glu Leu Pro Leu Ala Pro Gly Gly Ala Pro Leu 385 390 395 400				
20	Leu Ala Gly Val Ser Ser Phe Gly Ile Gly Gly Thr Asn Cys His Val 405 410 415				
	Val Leu Glu His Leu Pro Ser Arg Pro Thr Pro Ala Val Ser Val Ala 420 425 430				
25	Ala Ser Leu Pro Asp Val Pro Pro Leu Leu Leu Ser Ala Arg Ser Glu 435 440 445				
	Gly Ala Leu Arg Ala Gln Ala Val Arg Leu Gly Glu Tyr Val Glu Arg 450 455 460				
30	Val Gly Ala Asp Pro Arg Asp Val Ala Tyr Ser Leu Ala Ser Thr Arg 465 470 475 480				
	Thr Leu Phe Glu His Arg Ala Val Val Pro Cys Gly Gly Arg Gly Glu 485 490 495				
35	Leu Val Ala Ala Leu Gly Gly Phe Ala Ala Gly Arg Val Ser Gly Gly 500 505 510				
	Val Arg Ser Gly Arg Ala Val Pro Gly Gly Val Gly Val Leu Phe Thr 515 520 525				
40	Gly Gln Gly Ala Gln Trp Val Gly Met Gly Arg Gly Leu Tyr Ala Gly 530 535 540				
	Gly Gly Val Phe Ala Glu Val Leu Asp Glu Val Leu Ser Met Val Gly 545 550 555 560				
45	Glu Val Asp Gly Arg Ser Leu Arg Asp Val Met Phe Gly Asp Val Asp 565 570 575				
	Val Asp Ala Gly Ala Gly Ala Asp Ala Gly Ala Gly Ala Gly Ala Gly 580 585 590				
50	Val Gly Ser Gly Ser Gly Ser Val Gly Gly Leu Leu Gly Arg Thr Glu 595 600 605				
55	Phe Ala Gln Pro Ala Leu Phe Ala Leu Glu Val Ala Leu Phe Arg Ala 610 615 620				

EP 0 791 655 A2

Leu Glu Ala Arg Gly Val Glu Val Ser Val Val Leu Gly His Ser Val
 625 630 635 640
 5 Gly Glu Val Ala Ala Ala Tyr Val Ala Gly Val Leu Ser Leu Gly Asp
 645 650 655
 Ala Val Arg Leu Val Val Ala Arg Gly Gly Leu Met Gly Gly Leu Pro
 660 665 670
 10 Val Gly Gly Gly Met Trp Ser Val Gly Ala Ser Glu Ser Val Val Arg
 675 680 685
 Gly Val Val Glu Gly Leu Gly Glu Trp Val Ser Val Ala Ala Val Asn
 690 695 700
 15 Gly Pro Arg Ser Val Val Leu Ser Gly Asp Val Gly Val Leu Glu Ser
 705 710 715 720
 Val Val Ala Ser Leu Met Gly Asp Gly Val Glu Cys Arg Arg Leu Asp
 725 730 735
 20 Val Ser His Gly Phe His Ser Val Leu Met Glu Pro Val Leu Gly Glu
 740 745 750
 Phe Arg Gly Val Val Glu Ser Leu Glu Phe Gly Arg Val Arg Pro Gly
 755 760 765
 25 Val Val Val Val Ser Gly Val Ser Gly Gly Val Val Gly Ser Gly Glu
 770 775 780
 Leu Gly Asp Pro Gly Tyr Trp Val Arg His Ala Arg Glu Ala Val Arg
 785 790 795 800
 Phe Ala Asp Gly Val Gly Val Val Arg Gly Leu Gly Val Gly Thr Leu
 805 810 815
 35 Val Glu Val Gly Pro His Gly Val Leu Thr Gly Met Ala Gly Glu Cys
 820 825 830
 Leu Gly Ala Gly Asp Asp Val Val Val Val Pro Ala Met Arg Arg Gly
 835 840 845
 40 Arg Ala Glu Arg Glu Val Phe Glu Ala Ala Leu Ala Thr Val Phe Thr
 850 855 860
 Arg Asp Ala Gly Leu Asp Ala Thr Ala Leu His Thr Gly Ser Thr Gly
 865 870 875 880
 45 Arg Arg Ile Asp Leu Pro Thr Tyr Pro Phe Gln Arg Arg Thr His Trp
 885 890 895
 Ser Pro Ala Leu Ser Arg Pro Val Thr Ala Asp Ala Gly Ala Gly Val
 900 905 910
 50 Thr Ala Thr Asp Ala Val Gly His Ser Val Ser Pro Asp Pro Glu Ser
 915 920 925
 Thr Glu Gly Thr Ser His Arg Asp Thr Asp Asp Glu Ala Asp Ser Ala
 930 935 940
 55

EP 0 791 655 A2

	Ser Pro Glu Pro Met Ser Pro Glu Asp Ala Val Arg Leu Val Arg Glu	
	945	950 955 960
5	Ser Thr Ala Ala Val Leu Gly His Asp Asp Pro Gly Glu Val Ala Leu	
		965 970 975
	Asp Arg Thr Phe Thr Ser Gln Gly Met Asp Ser Val Thr Ala Val Glu	
		980 985 990
10	Leu Cys Asp Leu Leu Lys Gly Ala Ser Gly Leu Pro Leu Ala Ala Thr	
		995 1000 1005
	Leu Val Tyr Asp Leu Pro Thr Pro Arg Ala Val Ala Glu His Ile Val	
		1010 1015 1020
15	Glu Ala Ala Gly Gly Pro Lys Asp Ser Val Ala Gly Gly Pro Gly Val	
		1025 1030 1035 1040
	Leu Ser Ser Ala Ala Val Gly Val Ser Asp Ala Arg Gly Gly Ser Arg	
		1045 1050 1055
20	Asp Asp Asp Asp Pro Ile Ala Ile Val Gly Val Gly Cys Arg Leu Pro	
		1060 1065 1070
	Gly Gly Val Asp Ser Arg Ala Ala Leu Trp Glu Leu Leu Glu Ser Gly	
		1075 1080 1085
25	Ala Asp Ala Ile Ser Ser Phe Pro Thr Asp Arg Gly Trp Asp Leu Asp	
		1090 1095 1100
	Gly Leu Tyr Asp Pro Glu Pro Gly Thr Pro Gly Lys Thr Tyr Val Arg	
		1105 1110 1115 1120
30	Glu Gly Gly Phe Leu His Ser Ala Ala Glu Phe Asp Ala Glu Phe Phe	
		1125 1130 1135
	Gly Ile Ser Pro Arg Glu Ala Thr Ala Met Asp Pro Gln Gln Arg Leu	
		1140 1145 1150
35	Leu Leu Glu Ala Ser Trp Glu Ala Leu Glu Asp Ala Gly Val Leu Pro	
		1155 1160 1165
40	Glu Ser Leu Arg Gly Gly Asp Ala Gly Val Phe Val Gly Ala Thr Ala	
		1170 1175 1180
	Pro Glu Tyr Gly Pro Arg Leu His Glu Gly Ala Asp Gly Tyr Glu Gly	
		1185 1190 1195 1200
45	Tyr Leu Leu Thr Gly Thr Thr Ala Ser Val Ala Ser Gly Arg Ile Ala	
		1205 1210 1215
	Tyr Thr Leu Gly Thr Gly Gly Pro Ala Leu Thr Val Asp Thr Ala Cys	
		1220 1225 1230
50	Ser Ser Ser Leu Val Ala Leu His Leu Ala Val Gln Ala Leu Arg Arg	
		1235 1240 1245
	Gly Glu Cys Gly Leu Ala Leu Ala Gly Gly Ala Thr Val Met Ser Gly	
		1250 1255 1260
55	Pro Gly Met Phe Val Glu Phe Ser Arg Gln Arg Gly Leu Ala Pro Asp	

EP 0 791 655 A2

	1265	1270	1275	1280
	Gly Arg Cys Met	Pro Phe Ser Ala	Asp Ala Asp Gly Thr Ala	Trp Ser
		1285	1290	1295
5	Glu Gly Val	Ala Val Leu Ala Leu	Glu Arg Leu Ser Asp Ala Arg Arg	
		1300	1305	1310
	Ala Gly His Arg Val	Leu Gly Val Val Arg Gly Ser	Ala Val Asn Gln	
10		1315	1320	1325
	Asp Gly Ala Ser Asn Gly	Leu Thr Ala Pro Asn Arg Ser	Ala Gln Glu	
		1330	1335	1340
	Gly Val Ile Arg Ala	Ala Leu Ala Asp Ala Gly Leu Ala	Pro Gly Asp	
15		1345	1350	1355
	Val Asp Ala Val Glu	Ala His Gly Thr Gly Thr Ala Leu Gly	Asp Pro	
		1365	1370	1375
	Ile Glu Ala Ser Ala	Leu Leu Ala Thr Tyr Gly Arg Glu	Arg Val Gly	
20		1380	1385	1390
	Asp Pro Leu Trp Leu	Gly Ser Leu Lys Ser Asn Val Gly His Thr	Gln	
		1395	1400	1405
	Ala Ala Ala Gly Ala	Ala Gly Val Val Lys Met Leu Leu Ala Leu	Glu	
25		1410	1415	1420
	His Gly Thr Leu Pro	Arg Thr Leu His Ala Asp Arg Pro Ser Thr	His	
		1425	1430	1435
30		1440		
	Val Asp Trp Ser Ser	Gly Thr Val Ala Leu Leu Ala Glu Ala Arg Arg		
		1445	1450	1455
	Trp Pro Arg Arg Ser	Asp Arg Pro Arg Arg Ala Ala Val Ser Ser Phe		
35		1460	1465	1470
	Gly Ile Ser Gly Thr	Asn Ala His Leu Ile Ile Glu Glu Ala Pro Glu		
		1475	1480	1485
	Trp Val Glu Asp Ile	Asp Gly Val Ala Ala Pro Asp Arg Gly Thr Ala		
40		1490	1495	1500
	Asp Ala Ala Ala Pro	Ser Pro Leu Leu Leu Ser Ala Arg Ser Glu Gly		
		1505	1510	1515
	Ala Leu Arg Ala Gln	Ala Val Arg Leu Gly Glu Tyr Val Glu Arg Val		
45		1525	1530	1535
	Gly Ala Asp Pro Arg	Asp Val Ala Tyr Ser Leu Ala Ser Thr Arg Thr		
		1540	1545	1550
	Leu Phe Glu His Arg	Ala Val Val Pro Cys Gly Gly Arg Gly Glu Leu		
50		1555	1560	1565
	Val Ala Ala Leu Gly	Gly Phe Ala Ala Gly Arg Val Ser Gly Gly Val		
		1570	1575	1580
	Arg Ser Gly Arg Ala	Val Pro Gly Gly Val Gly Val Leu Phe Thr Gly		
55		1585	1590	1595
				1600

EP 0 791 655 A2

Gln Gly Ala Gln Trp Val Gly Met Gly Arg Gly Leu Tyr Ala Gly Gly
 1605 1610 1615
 5 Gly Val Phe Ala Glu Val Leu Asp Glu Val Leu Ser Met Val Gly Glu
 1620 1625 1630
 Val Asp Gly Arg Ser Leu Arg Asp Val Met Phe Gly Asp Val Asp Val
 1635 1640 1645
 10 Asp Ala Gly Ala Gly Ala Asp Ala Gly Ala Gly Ala Gly Ala Gly Val
 1650 1655 1660
 Gly Ser Gly Ser Gly Ser Val Gly Gly Leu Leu Gly Arg Thr Glu Phe
 1665 1670 1675 1680
 15 Ala Gln Pro Ala Leu Phe Ala Leu Glu Val Ala Leu Phe Arg Ala Leu
 1685 1690 1695
 Glu Ala Arg Gly Val Glu Val Ser Val Val Leu Gly His Ser Val Gly
 1700 1705 1710
 20 Glu Val Ala Ala Ala Tyr Val Ala Gly Val Leu Ser Leu Gly Asp Ala
 1715 1720 1725
 Val Arg Leu Val Val Ala Arg Gly Gly Leu Met Gly Gly Leu Pro Val
 1730 1735 1740
 25 Gly Gly Gly Met Trp Ser Val Gly Ala Ser Glu Ser Val Val Arg Gly
 1745 1750 1755 1760
 Val Val Glu Gly Leu Gly Glu Trp Val Ser Val Ala Ala Val Asn Gly
 1765 1770 1775
 Pro Arg Ser Val Val Leu Ser Gly Asp Val Gly Val Leu Glu Ser Val
 1780 1785 1790
 35 Val Ala Ser Leu Met Gly Asp Gly Val Glu Cys Arg Arg Leu Asp Val
 1795 1800 1805
 Ser His Gly Phe His Ser Val Leu Met Glu Pro Val Leu Gly Glu Phe
 1810 1815 1820
 40 Arg Gly Val Val Glu Ser Leu Glu Phe Gly Arg Val Arg Pro Gly Val
 1825 1830 1835 1840
 Val Val Val Ser Gly Val Ser Gly Gly Val Val Gly Ser Gly Glu Leu
 1845 1850 1855
 45 Gly Asp Pro Gly Tyr Trp Val Arg His Ala Arg Glu Ala Val Arg Phe
 1860 1865 1870
 Ala Asp Gly Val Gly Val Val Arg Gly Leu Gly Val Gly Thr Leu Val
 1875 1880 1885
 50 Glu Val Gly Pro His Gly Val Leu Thr Gly Met Ala Gly Glu Cys Leu
 1890 1895 1900
 Gly Ala Gly Asp Asp Val Val Val Val Pro Ala Met Arg Arg Gly Arg
 1905 1910 1915 1920
 55

EP 0 791 655 A2

Ala Glu Arg Glu Val Phe Glu Ala Ala Leu Ala Thr Val Phe Thr Arg
1925 1930 1935

5 Asp Ala Gly Leu Asp Ala Thr Ala Leu His Thr Gly Ser Thr Gly Arg
1940 1945 1950

Arg Ile Asp Leu Pro Thr Tyr Pro Phe Gln Arg Asp Arg Tyr Trp Leu
1955 1960 1965

10 Asp Pro Val Arg Thr Ala Val Thr Gly Val Glu Pro Ala Gly Ser Pro
1970 1975 1980

Ala Asp Ala Arg Ala Thr Glu Arg Gly Arg Ser Thr Thr Ala Gly Ile
1985 1990 1995 2000

15 Arg Tyr Arg Val Ala Trp Gln Pro Ala Val Val Asp Arg Gly Asn Pro
2005 2010 2015

Gly Pro Ala Gly His Val Leu Leu Leu Ala Pro Asp Glu Asp Thr Ala
2020 2025 2030

20 Asp Ser Gly Leu Ala Pro Ala Ile Ala Arg Glu Leu Ala Val Arg Gly
2035 2040 2045

Ala Glu Val His Thr Val Ala Val Pro Val Gly Thr Gly Arg Glu Ala
2050 2055 2060

25 Ala Gly Asp Leu Leu Arg Ala Ala Gly Asp Gly Ala Ala Arg Ser Thr
2065 2070 2075 2080

Arg Val Leu Trp Leu Ala Pro Ala Glu Pro Asp Ala Ala Asp Ala Val
2085 2090 2095

30 Ala Leu Val Gln Ala Leu Gly Glu Ala Val Pro Glu Ala Pro Leu Trp
2100 2105 2110

Ile Thr Thr Arg Glu Ala Ala Ala Val Arg Pro Asp Glu Thr Pro Ser
2115 2120 2125

35 Val Gly Gly Ala Gln Leu Trp Gly Leu Gly Gln Val Ala Ala Leu Glu
2130 2135 2140

Leu Gly Arg Arg Trp Gly Gly Leu Ala Asp Leu Pro Gly Ser Ala Ser
2145 2150 2155 2160

Pro Ala Val Leu Arg Thr Phe Val Gly Ala Leu Leu Ala Gly Gly Glu
2165 2170 2175

45 Asn Gln Phe Ala Val Arg Pro Ser Gly Val His Val Arg Arg Val Val
2180 2185 2190

Pro Ala Pro Val Pro Val Pro Ala Ser Ala Arg Thr Val Thr Thr Ala
2195 2200 2205

50 Pro Ala Thr Ala Val Gly Glu Asp Ala Arg Asn Asp Thr Ser Asp Val
2210 2215 2220

Val Val Pro Asp Asp Arg Trp Ser Ser Gly Thr Val Leu Ile Thr Gly
2225 2230 2235 2240

55

EP 0 791 655 A2

Gly Thr Gly Ala Leu Gly Ala Gln Val Ala Arg Arg Leu Ala Arg Ser
 2245 2250 2255
 Gly Ala Ala Arg Leu Leu Leu Val Gly Arg Arg Gly Ala Ala Gly Pro
 2260 2265 2270
 5
 Gly Val Gly Glu Leu Val Glu Glu Leu Thr Ala Leu Gly Ser Glu Val
 2275 2280 2285
 Ala Val Glu Ala Cys Asp Val Ala Asp Arg Asp Ala Leu Ala Ala Leu
 2290 2295 2300
 10
 Leu Ala Gly Leu Pro Glu Glu Arg Pro Leu Val Ala Val Leu His Ala
 2305 2310 2315 2320
 Ala Gly Val Leu Asp Asp Gly Val Leu Asp Ser Leu Thr Ser Asp Arg
 2325 2330 2335
 15
 Val Asp Ala Val Leu Arg Asp Lys Val Thr Ala Ala Arg His Leu Asp
 2340 2345 2350
 Glu Leu Thr Ala Asp Leu Pro Leu Asp Ala Phe Val Leu Phe Ser Ser
 2355 2360 2365
 20
 Ile Val Gly Val Trp Gly Asn Gly Gly Gln Ala Val Tyr Ala Ala Ala
 2370 2375 2380
 25
 Asn Ala Ala Leu Asp Ala Leu Ala Gln Arg Arg Arg Ala Arg Gly Ala
 2385 2390 2395 2400
 Arg Ala Ala Ser Ile Ala Trp Gly Pro Trp Ala Gly Ala Gly Met Ala
 2405 2410 2415
 30
 Ser Gly Thr Ala Ala Lys Ser Phe Glu Arg Asp Gly Val Thr Ala Leu
 2420 2425 2430
 Asp Pro Glu Arg Ala Leu Asp Val Leu Asp Asp Val Val Gly Ala Gly
 2435 2440 2445
 35
 Gly Thr Ser Ala Ala Gly Thr His Ala Ala Gly Glu Ser Ser Leu Leu
 2450 2455 2460
 Val Ala Asp Val Asp Trp Glu Thr Phe Val Gly Arg Ser Val Thr Arg
 2465 2470 2475 2480
 40
 Arg Thr Trp Ser Leu Phe Asp Gly Val Ser Ala Ala Arg Ser Ala Arg
 2485 2490 2495
 Ala Gly His Ala Ala Asp Asp Arg Ala Ala Leu Thr Pro Gly Thr Arg
 2500 2505 2510
 45
 Pro Gly Asp Gly Ala Pro Gly Gly Ser Gly Gln Asp Gly Gly Glu Gly
 2515 2520 2525
 50
 Arg Pro Trp Leu Ser Val Gly Pro Ser Pro Ala Glu Arg Arg Arg Ala
 2530 2535 2540
 Leu Leu Thr Leu Val Arg Ser Glu Ala Ala Gly Ile Leu Arg His Ala
 2545 2550 2555 2560
 55
 Ser Ala Asp Ala Val Asp Pro Glu Leu Ala Phe Arg Ser Ala Gly Phe

EP 0 791 655 A2

	2565	2570	2575
5	Asp Ser Leu Thr Val Leu Glu Leu Arg Asn Arg Leu Thr Ala Ala Thr 2580	2585	2590
	Gly Leu Asn Leu Pro Asn Thr Leu Leu Phe Asp His Pro Thr Pro Leu 2595	2600	2605
	Ser Leu Ala Ser His Leu His Asp Glu Leu Phe Gly Pro Asp Ser Glu 2610	2615	2620
10	Ala Glu Pro Ala Ala Ala Ala Pro Thr Pro Val Met Ala Asp Glu Arg 2625	2630	2635 2640
	Glu Pro Ile Ala Ile Val Gly Met Ala Cys Arg Tyr Pro Gly Gly Val 2645	2650	2655
15	Ala Ser Pro Asp Asp Leu Trp Asp Leu Val Ala Gly Asp Gly His Thr 2660	2665	2670
	Leu Ser Pro Phe Pro Ala Asp Arg Gly Trp Asp Val Glu Gly Leu Tyr 2675	2680	2685
20	Asp Pro Glu Pro Gly Val Pro Gly Lys Ser Tyr Val Arg Glu Gly Gly 2690	2695	2700
	Phe Leu Arg Ser Ala Ala Glu Phe Asp Ala Glu Phe Phe Gly Ile Ser 2705	2710	2715 2720
	Pro Arg Glu Ala Thr Ala Met Asp Pro Gln Gln Arg Leu Leu Leu Glu 2725	2730	2735
30	Thr Ser Trp Glu Ala Leu Glu Arg Ala Gly Ile Val Pro Asp Ser Leu 2740	2745	2750
	Arg Gly Thr Arg Thr Gly Val Phe Ser Gly Ile Ser Gln Gln Asp Tyr 2755	2760	2765
35	Ala Thr Gln Leu Gly Asp Ala Ala Asp Thr Tyr Gly Gly His Val Leu 2770	2775	2780
	Thr Gly Thr Leu Gly Ser Val Ile Ser Gly Arg Val Ala Tyr Ala Leu 2785	2790	2795 2800
40	Gly Leu Glu Gly Pro Ala Leu Thr Val Asp Thr Ala Cys Ser Ser Ser 2805	2810	2815
	Leu Val Ala Leu His Leu Ala Val Gln Ser Leu Arg Arg Gly Glu Cys 2820	2825	2830
45	Asp Leu Ala Leu Ala Gly Gly Val Thr Val Met Ala Thr Pro Thr Val 2835	2840	2845
	Phe Val Glu Phe Ser Arg Gln Arg Gly Leu Ala Ala Asp Gly Arg Cys 2850	2855	2860
50	Lys Ala Phe Ala Glu Gly Ala Asp Gly Thr Ala Trp Ala Glu Gly Val 2865	2870	2875 2880
	Gly Val Leu Leu Val Glu Arg Leu Ser Asp Ala Arg Arg Asn Gly His 2885	2890	2895
55			

Arg Val Leu Ala Val Val Arg Gly Ser Ala Val Asn Gln Asp Gly Ala
 2900 2905 2910
 5 Ser Asn Gly Leu Thr Ala Pro Ser Gly Pro Ala Gln Gln Arg Val Ile
 2915 2920 2925
 Arg Glu Ala Leu Ala Asp Ala Gly Leu Val Pro Ala Asp Val Asp Val
 2930 2935 2940
 10 Val Glu Ala His Gly Thr Gly Thr Ala Leu Gly Asp Pro Ile Glu Ala
 2945 2950 2955 2960
 Gly Ala Leu Leu Ala Thr Tyr Gly Arg Glu Arg Val Gly Asp Pro Leu
 2965 2970 2975
 15 Trp Leu Gly Ser Leu Lys Ser Asn Ile Gly His Ala Gln Ala Ala Ala
 2980 2985 2990
 Gly Val Gly Gly Val Ile Lys Val Val Gln Gly Met Arg His Gly Ser
 2995 3000 3005
 20 Leu Pro Arg Thr Leu His Val Asp Ala Pro Ser Ser Lys Val Glu Trp
 3010 3015 3020
 Ala Ser Gly Ala Val Glu Leu Leu Thr Glu Thr Arg Ser Trp Pro Arg
 3025 3030 3035 3040
 25 Arg Val Glu Arg Val Arg Arg Ala Ala Val Ser Ala Phe Gly Val Ser
 3045 3050 3055
 Gly Thr Asn Ala His Val Val Leu Glu Glu Ala Pro Ala Glu Ala Gly
 3060 3065 3070
 30 Ser Glu His Gly Asp Gly Pro Glu Pro Glu Arg Pro Asp Ala Val Thr
 3075 3080 3085
 Gly Pro Leu Ser Trp Val Leu Ser Ala Arg Ser Glu Gly Ala Leu Arg
 3090 3095 3100
 35 Ala Gln Ala Val Arg Leu Arg Glu Cys Val Glu Arg Val Gly Ala Asp
 3105 3110 3115 3120
 40 Pro Arg Asp Val Ala Gly Ser Leu Val Val Ser Arg Ala Ser Phe Gly
 3125 3130 3135
 Glu Arg Ala Val Val Val Gly Arg Gly Arg Glu Glu Leu Leu Ala Gly
 3140 3145 3150
 45 Leu Asp Val Val Ala Ala Gly Ala Pro Val Gly Val Ser Ser Gly Ala
 3155 3160 3165
 Gly Ala Val Val Arg Gly Ser Ala Val Arg Gly Arg Gly Val Gly Val
 3170 3175 3180
 50 Leu Phe Thr Gly Gln Gly Ala Gln Trp Val Gly Met Gly Arg Gly Leu
 3185 3190 3195 3200
 Tyr Ala Gly Gly Gly Val Phe Ala Glu Val Leu Asp Glu Val Leu Ser
 3205 3210 3215
 55

EP 0 791 655 A2

Val Val Gly Glu Val Asp Gly Arg Ser Leu Arg Asp Val Met Phe Ala
3220 3225 3230

5 Asp Ala Asp Ser Val Leu Gly Gly Leu Leu Gly Arg Thr Glu Phe Ala
3235 3240 3245

Gln Pro Ala Leu Phe Ala Leu Glu Val Ala Leu Phe Arg Ala Leu Glu
3250 3255 3260

10 Ala Arg Gly Val Glu Val Ser Val Val Leu Gly His Ser Val Gly Glu
3265 3270 3275 3280

Val Ala Ala Ala Tyr Val Ala Gly Val Leu Ser Leu Gly Asp Ala Val
3285 3290 3295

15 Arg Leu Val Val Ala Arg Gly Gly Leu Met Gly Gly Leu Pro Val Gly
3300 3305 3310

Gly Gly Met Trp Ser Val Gly Ala Ser Glu Ser Val Val Arg Gly Val
3315 3320 3325

20 Val Glu Gly Leu Gly Glu Trp Val Ser Val Ala Ala Val Asn Gly Pro
3330 3335 3340

Arg Ser Val Val Leu Ser Gly Asp Val Gly Val Leu Glu Ser Val Val
3345 3350 3355 3360

25 Val Thr Leu Met Gly Asp Gly Val Glu Cys Arg Arg Leu Asp Val Ser
3365 3370 3375

His Gly Phe His Ser Val Leu Met Glu Pro Val Leu Gly Glu Phe Arg
3380 3385 3390

30 Gly Val Val Glu Ser Leu Glu Phe Gly Arg Val Arg Pro Gly Val Val
3395 3400 3405

Val Val Ser Gly Val Ser Gly Gly Val Val Gly Ser Gly Glu Leu Gly
3410 3415 3420

35 Asp Pro Gly Tyr Trp Val Arg His Ala Arg Glu Ala Val Arg Phe Ala
3425 3430 3435 3440

40 Asp Gly Val Gly Val Val Arg Gly Leu Gly Val Gly Thr Leu Val Glu
3445 3450 3455

Val Gly Pro His Gly Val Leu Thr Gly Met Ala Gly Gln Cys Leu Glu
3460 3465 3470

45 Ala Gly Asp Asp Val Val Val Val Pro Ala Met Arg Arg Gly Arg Pro
3475 3480 3485

Glu Arg Glu Val Phe Glu Ala Ala Leu Ala Thr Val Phe Thr Arg Asp
3490 3495 3500

50 Ala Gly Leu Asp Ala Thr Thr Leu His Thr Gly Ser Thr Gly Arg Arg
3505 3510 3515 3520

Ile Asp Leu Pro Thr Tyr Pro Phe Gln His Asn Arg Tyr Trp Ala Thr
3525 3530 3535

55 Gly Ser Val Thr Gly Ala Thr Gly Thr Ser Ala Ala Ala Arg Phe Gly

EP 0 791 655 A2

	3540	3545	3550
5	Leu Glu Trp Lys Asp His Pro Phe Leu Ser Gly Ala Thr Pro Ile Ala 3555 3560 3565		
	Gly Ser Gly Ala Leu Leu Leu Thr Gly Arg Val Gly Leu Ala Ala His 3570 3575 3580		
10	Pro Trp Leu Ala Asp His Ala Ile Ser Gly Thr Val Leu Leu Pro Gly 3585 3590 3595 3600		
	Thr Ala Ile Ala Asp Leu Leu Leu Arg Ala Val Glu Glu Val Gly Ala 3605 3610 3615		
15	Gly Gly Val Glu Glu Leu Thr Leu His Glu Pro Leu Leu Leu Pro Glu 3620 3625 3630		
	Arg Gly Gly Leu His Val Gln Val Leu Val Glu Ala Ala Asp Glu Gln 3635 3640 3645		
20	Gly Arg Arg Ala Val Ala Val Ala Ala Arg Pro Glu Gly Pro Gly Arg 3650 3655 3660		
	Asp Gly Glu Glu Gln Glu Trp Thr Arg His Ala Glu Gly Val Leu Thr 3665 3670 3675 3680		
25	Ser Thr Glu Thr Ala Val Pro Asp Met Gly Trp Ala Ala Gly Ala Trp 3685 3690 3695		
	Pro Pro Pro Gly Ala Glu Pro Ile Asp Val Glu Glu Leu Tyr Asp Ala 3700 3705 3710		
30	Phe Ala Ala Asp Gly Tyr Gly Tyr Gly Pro Ala Phe Thr Ala Leu Ser 3715 3720 3725		
	Gly Val Trp Arg Leu Gly Asp Glu Leu Phe Ala Glu Val Arg Arg Pro 3730 3735 3740		
35	Ala Gly Gly Ala Gly Thr Thr Gly Asp Gly Phe Gly Val His Pro Ala 3745 3750 3755 3760		
	Leu Phe Asp Ala Ala Leu His Pro Trp Arg Ala Gly Gly Leu Leu Pro 3765 3770 3775		
40	Asp Thr Gly Gly Thr Thr Trp Ala Pro Phe Ser Trp Gln Gly Ile Ala 3780 3785 3790		
	Leu His Thr Thr Gly Ala Glu Thr Leu Arg Val Arg Leu Ala Pro Ala 3795 3800 3805		
45	Ala Gly Gly Thr Glu Ser Ala Phe Ser Val Gln Ala Ala Asp Pro Ala 3810 3815 3820		
	Gly Thr Pro Val Leu Thr Leu Asp Ala Leu Leu Leu Arg Pro Val Thr 3825 3830 3835 3840		
50	Leu Gly Arg Ala Asp Ala Pro Gln Pro Leu Tyr Arg Val Asp Trp Gln 3845 3850 3855		
55	Pro Val Gly Gln Gly Thr Glu Ala Ser Gly Ala Gln Gly Trp Thr Val 3860 3865 3870		

EP 0 791 655 A2

Leu Gly Gln Ala Ala Ala Glu Thr Val Ala Gln Pro Ala Ala His Ala
 3875 3880 3885
 5 Asp Leu Thr Ala Leu Arg Thr Ala Val Ala Ala Gly Thr Pro Val
 3890 3895 3900
 Pro Arg Leu Val Val Val Ser Pro Val Asp Thr Arg Leu Asp Glu Gly
 3905 3910 3915 3920
 10 Pro Val Leu Ala Asp Ala Glu Ala Arg Ala Arg Ala Gly Asp Gly Trp
 3925 3930 3935
 Asp Asp Asp Pro Leu Arg Val Ala Leu Gly Arg Gly Leu Thr Leu Val
 3940 3945 3950
 15 Arg Glu Trp Val Glu Asp Glu Arg Leu Ala Asp Ser Arg Leu Val Val
 3955 3960 3965
 Leu Thr Arg Gly Ala Val Ala Ala Gly Pro Gly Asp Val Pro Asp Leu
 3970 3975 3980
 20 Thr Gly Ala Ala Leu Trp Gly Leu Leu Arg Ser Ala Gln Ser Glu Tyr
 3985 3990 3995 4000
 25 Pro Asp Arg Phe Thr Leu Ile Asp Val Asp Asp Ser Pro Glu Ser Arg
 4005 4010 4015
 Ala Ala Leu Pro Arg Ala Leu Gly Ser Ala Glu Arg Gln Leu Ala Leu
 4020 4025 4030
 Arg Thr Gly Asp Val Leu Ala Pro Ala Leu Val Pro Met Ala Thr Arg
 4035 4040 4045
 30 Pro Ala Glu Thr Thr Pro Ala Thr Ala Val Ala Ser Ala Thr Thr Gln
 4050 4055 4060
 35 Thr Gln Val Thr Ala Pro Ala Pro Asp Asp Pro Ala Ala Asp Ala Val
 4065 4070 4075 4080
 Phe Asp Pro Ala Gly Thr Val Leu Ile Thr Gly Gly Thr Gly Ala Leu
 4085 4090 4095
 40 Gly Arg Arg Val Ala Ser His Leu Ala Arg Arg Tyr Gly Val Arg His
 4100 4105 4110
 Met Leu Leu Val Ser Arg Arg Gly Pro Asp Ala Pro Glu Ala Gly Pro
 4115 4120 4125
 45 Leu Glu Arg Glu Leu Ala Gly Leu Gly Val Thr Ala Thr Phe Leu Ala
 4130 4135 4140
 Cys Asp Leu Thr Asp Ile Glu Ala Val Arg Lys Ala Val Ala Ala Val
 4145 4150 4155 4160
 50 Pro Ser Asp His Pro Leu Thr Gly Val Val His Thr Ala Gly Val Leu
 4165 4170 4175
 Asp Asp Gly Ala Leu Thr Gly Leu Thr Arg Gln Arg Leu Asp Thr Val
 4180 4185 4190
 55

EP 0 791 655 A2

Leu Arg Pro Lys Ala Asp Ala Val Arg Asn Leu His Glu Ala Thr Leu
4195 4200 4205

5 Asp Arg Pro Leu Arg Ala Phe Val Leu Phe Ser Ala Ala Ala Gly Leu
4210 4215 4220

Leu Gly Arg Pro Gly Gln Ala Ser Tyr Ala Ala Ala Asn Ala Val Leu
4225 4230 4235 4240

10 Asp Ala Leu Ala Gly Ala Arg Arg Ala Ala Gly Leu Pro Ala Val Ser
4245 4250 4255

Leu Ala Trp Gly Leu Trp Asp Glu Gln Thr Gly Met Ala Gly Gly Leu
4260 4265 4270

15 Asp Glu Met Ala Leu Arg Val Leu Arg Arg Asp Gly Ile Ala Ala Met
4275 4280 4285

Pro Pro Glu Gln Gly Leu Glu Leu Leu Asp Leu Ala Leu Thr Gly His
4290 4295 4300

20 Arg Asp Gly Pro Ala Val Leu Val Pro Leu Leu Leu Asp Gly Ala Ala
4305 4310 4315 4320

Leu Arg Arg Thr Ala Lys Glu Arg Gly Ala Ala Thr Met Ser Pro Leu
4325 4330 4335

25 Leu Arg Ala Leu Leu Pro Ala Ala Leu Arg Arg Ser Gly Gly Ala Gly
4340 4345 4350

Ala Pro Ala Ala Ala Asp Arg His Gly Lys Glu Ala Asp Pro Gly Ala
4355 4360 4365

30 Gly Arg Leu Ala Gly Met Val Ala Leu Glu Ala Ala Glu Arg Ser Ala
4370 4375 4380

Ala Val Leu Glu Leu Val Thr Glu Gln Val Ala Glu Val Leu Gly Tyr
4385 4390 4395 4400

35 Ala Ser Ala Ala Glu Ile Glu Pro Glu Arg Pro Phe Arg Glu Ile Gly
4405 4410 4415

Val Asp Ser Leu Ala Ala Val Glu Leu Arg Asn Arg Leu Ser Arg Leu
4420 4425 4430

40 Val Gly Leu Arg Leu Pro Thr Thr Leu Ser Phe Asp His Pro Thr Pro
4435 4440 4445

Lys Asp Met Ala Gln His Ile Asp Gly Gln Leu Pro Arg Pro Ala Gly
4450 4455 4460

Ala Ser Pro Ala Asp Ala Ala Leu Glu Gly Ile Gly Asp Leu Ala Arg
4465 4470 4475 4480

50 Ala Val Ala Leu Leu Gly Thr Gly Asp Ala Arg Arg Ala Glu Val Arg
4485 4490 4495

Glu Gln Leu Val Gly Leu Leu Ala Ala Leu Asp Pro Pro Gly Arg Thr
4500 4505 4510

55 Gly Thr Ala Ala Pro Gly Val Pro Ser Gly Ala Asp Gly Ala Glu Pro

4515

4520

4525

Thr Val Thr Asp Arg Leu Asp Glu Ala Thr Asp Asp Glu Ile Phe Ala,
 4530 4535 4540

Phe Leu Asp Glu Gln Leu
 4545 4550

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1996 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Thr Ala Glu Asn Asp Lys Ile Arg Ser Tyr Leu Lys Arg Ala Thr
 1 5 10 15
 Ala Glu Leu His Arg Thr Lys Ser Arg Leu Ala Glu Val Glu Ser Ala
 20 25 30
 Ser Arg Glu Pro Ile Ala Ile Val Gly Met Ala Cys Arg Tyr Pro Gly
 35 40 45
 Gly Val Ala Ser Pro Asp Asp Leu Trp Asp Leu Val Ala Ala Gly Thr
 50 55 60
 Asp Ala Val Ser Ala Phe Pro Val Asp Arg Gly Trp Asp Val Glu Gly
 65 70 75 80
 Leu Tyr Asp Pro Asp Pro Glu Ala Val Gly Arg Ser Tyr Val Arg Glu
 85 90 95
 Gly Gly Phe Leu His Ser Ala Ala Glu Phe Asp Ala Glu Phe Phe Gly
 100 105 110
 Ile Ser Pro Arg Glu Ala Ala Ala Met Asp Pro Gln Gln Arg Leu Leu
 115 120 125
 Leu Glu Thr Ser Trp Glu Ala Leu Glu Arg Ala Gly Ile Val Pro Ala
 130 135 140
 Ser Leu Arg Gly Thr Arg Thr Gly Val Phe Thr Gly Val Met Tyr Asp
 145 150 155 160
 Asp Tyr Gly Ser Arg Phe Asp Ser Ala Pro Pro Glu Tyr Glu Gly Tyr
 165 170 175
 Leu Val Asn Gly Ser Ala Gly Ser Ile Ala Ser Gly Arg Val Ala Tyr
 180 185 190
 Ala Leu Gly Leu Glu Gly Pro Ala Leu Thr Val Asp Thr Ala Cys Ser
 195 200 205
 Ser Ser Leu Val Ala Leu His Leu Ala Val Gln Ser Leu Arg Arg Gly

EP 0 791 655 A2

	210	215	220
5	Glu Cys Asp Leu Ala Leu Ala Gly Gly Val Thr Val Met Ala Thr Pro 225 230 235 240		
	Thr Val Leu Val Glu Phe Ser Arg Gln Arg Gly Leu Ala Ala Asp Gly 245 250 255		
10	Arg Cys Lys Ala Phe Ala Glu Gly Ala Asp Gly Thr Ala Trp Ala Glu 260 265 270		
	Gly Val Gly Val Leu Leu Val Glu Arg Leu Ser Asp Ala Arg Arg Asn 275 280 285		
15	Gly His Arg Val Leu Ala Val Val Arg Gly Ser Ala Val Asn Gln Asp 290 295 300		
	Gly Ala Ser Asn Gly Leu Thr Ala Pro Ser Gly Pro Ala Gln Gln Arg 305 310 315 320		
20	Val Ile Arg Glu Ala Leu Ala Asp Ala Gly Leu Thr Pro Ala Asp Val 325 330 335		
	Asp Ala Val Glu Ala His Gly Thr Gly Thr Pro Leu Gly Asp Pro Ile 340 345 350		
25	Glu Ala Gly Ala Leu Leu Ala Thr Tyr Gly Ser Glu Arg Gln Gly Gln 355 360 365		
	Gly Pro Leu Trp Leu Gly Ser Leu Lys Ser Asn Ile Gly His Ala Gln 370 375 380		
30	Ala Ala Ala Gly Val Gly Gly Val Ile Lys Val Val Gln Ala Met Arg 385 390 395 400		
	His Gly Ser Leu Pro Arg Thr Leu His Val Asp Ala Pro Ser Ser Lys 405 410 415		
35	Val Glu Trp Ala Ser Gly Ala Val Glu Leu Leu Thr Glu Thr Arg Ser 420 425 430		
	Trp Pro Arg Arg Val Glu Arg Val Arg Arg Ala Ala Val Ser Ala Phe 435 440 445		
40	Gly Val Ser Gly Thr Asn Ala His Val Val Leu Glu Glu Ala Pro Ala 450 455 460		
	Glu Ala Gly Ser Glu His Gly Asp Gly Pro Glu Pro Glu Arg Pro Asp 465 470 475 480		
45	Ala Val Thr Gly Pro Leu Ser Trp Val Leu Ser Ala Arg Ser Glu Gly 485 490 495		
	Ala Leu Arg Ala Gln Ala Val Arg Leu Arg Glu Cys Val Glu Arg Val 500 505 510		
50	Gly Ala Asp Pro Arg Asp Val Ala Gly Ser Leu Val Val Ser Arg Ala 515 520 525		
	Ser Phe Gly Glu Arg Ala Val Val Val Gly Arg Gly Arg Glu Glu Leu 530 535 540		

EP 0 791 655 A2

5 Leu Ala Gly Leu Asp Val Val Ala Ala Gly Ala Pro Val Gly Val Ser
 545 550 555 560
 Gly Gly Val Ser Ser Gly Ala Gly Ala Val Val Arg Gly Ser Ala Val
 565 570 575
 Arg Gly Arg Gly Val Gly Val Leu Phe Thr Gly Gln Gly Ala Gln Trp
 580 585 590
 10 Val Gly Met Gly Arg Gly Leu Tyr Ala Gly Gly Gly Val Phe Ala Glu
 595 600 605
 Val Leu Asp Glu Val Leu Ser Val Val Gly Glu Val Gly Gly Trp Ser
 610 615 620
 15 Leu Arg Asp Val Met Phe Gly Asp Val Asp Val Asp Ala Gly Ala Gly
 625 630 635 640
 Ala Asp Ala Gly Val Gly Ser Gly Val Gly Val Gly Gly Leu Leu Gly
 645 650 655
 20 Arg Thr Glu Phe Ala Gln Pro Ala Leu Phe Ala Leu Glu Val Ala Leu
 660 665 670
 Phe Arg Ala Leu Glu Ala Arg Gly Val Glu Val Ser Val Val Leu Gly
 675 680 685
 25 His Ser Val Gly Glu Val Ala Ala Ala Tyr Val Ala Gly Val Leu Ser
 690 695 700
 30 Leu Gly Asp Ala Val Arg Leu Val Val Ala Arg Gly Gly Leu Met Gly
 705 710 715 720
 Gly Leu Pro Val Gly Gly Gly Met Trp Ser Val Gly Ala Ser Glu Ser
 725 730 735
 35 Val Val Arg Gly Val Val Glu Gly Leu Gly Glu Trp Val Ser Val Ala
 740 745 750
 Ala Val Asn Gly Pro Arg Ser Val Val Leu Ser Gly Asp Val Gly Val
 755 760 765
 40 Leu Glu Ser Val Val Ala Ser Leu Met Gly Asp Gly Val Glu Cys Arg
 770 775 780
 Arg Leu Asp Val Ser His Gly Phe His Ser Val Leu Met Glu Pro Val
 785 790 795 800
 45 Leu Gly Glu Phe Arg Gly Val Val Glu Ser Leu Glu Phe Gly Arg Val
 805 810 815
 Arg Pro Gly Val Val Val Val Ser Ser Val Ser Gly Gly Val Val Gly
 820 825 830
 50 Ser Gly Glu Leu Gly Asp Pro Gly Tyr Trp Val Arg His Ala Arg Glu
 835 840 845
 55 Ala Val Arg Phe Ala Asp Gly Val Gly Val Val Arg Gly Leu Gly Val
 850 855 860

EP 0 791 655 A2

	Gly Thr Leu Val Glu Val Gly Pro His Gly Val Leu Thr Gly Met Ala	
	865	870 875 880
5	Gly Glu Cys Leu Gly Ala Gly Asp Asp Val Val Val Val Pro Ala Met	
		885 890 895
	Arg Arg Gly Arg Ala Glu Arg Glu Val Phe Glu Ala Ala Leu Ala Thr	
		900 905 910
10	Val Phe Thr Arg Asp Ala Gly Leu Asp Ala Thr Thr Leu His Thr Gly	
		915 920 925
	Ser Thr Gly Arg Arg Ile Asp Leu Pro Thr Tyr Pro Phe Gln His Asp	
		930 935 940
15	Arg Tyr Trp Leu Ala Ala Pro Ser Arg Pro Arg Thr Asp Gly Leu Ser	
		945 950 955 960
	Ala Ala Gly Leu Arg Glu Val Glu His Pro Leu Leu Thr Ala Ala Val	
		965 970 975
20	Glu Leu Pro Gly Thr Asp Thr Glu Val Trp Thr Gly Arg Ile Ser Ala	
		980 985 990
	Ala Asp Leu Pro Trp Leu Ala Asp His Leu Val Trp Asp Arg Gly Val	
		995 1000 1005
25	Val Pro Gly Thr Ala Leu Leu Glu Thr Val Leu Gln Val Gly Ser Arg	
		1010 1015 1020
	Ile Gly Leu Pro Arg Val Ala Glu Leu Val Leu Glu Thr Pro Leu Thr	
		1025 1030 1035 1040
30	Trp Thr Ser Asp Arg Pro Leu Gln Val Arg Ile Val Val Thr Ala Ala	
		1045 1050 1055
	Ala Thr Ala Pro Gly Gly Ala Arg Glu Leu Thr Leu His Ser Arg Pro	
		1060 1065 1070
35	Glu Pro Val Ala Ala Ser Ser Ser Ser Pro Ser Pro Ala Ser Pro Arg	
		1075 1080 1085
40	His Leu Thr Ala Gln Glu Ser Asp Asp Asp Trp Thr Arg His Ala Ser	
		1090 1095 1100
	Gly Leu Leu Ala Pro Ala Ala Gly Leu Ala Asp Asp Phe Ala Glu Leu	
		1105 1110 1115 1120
45	Thr Gly Ala Trp Pro Pro Val Gly Ala Glu Pro Leu Asp Leu Ala Gly	
		1125 1130 1135
	Gln Tyr Pro Leu Phe Ala Ala Ala Gly Val Arg Tyr Glu Gly Ala Phe	
		1140 1145 1150
50	Arg Gly Leu Arg Ala Ala Trp Arg Arg Gly Asp Glu Val Phe Ala Asp	
		1155 1160 1165
	Val Arg Leu Pro Asp Ala His Ala Val Asp Ala Asp Arg Tyr Gly Val	
		1170 1175 1180
55	His Pro Ala Leu Leu Asp Ala Val Leu His Pro Ile Ala Ser Leu Asp	

EP 0 791 655 A2

	1185		1190		1195		1200
	Pro Leu Gly Asp Gly Gly His Gly Leu Leu Pro Phe Ser Trp Thr Asp						
		1205			1210		1215
5	Val Gln Gly His Gly Ala Gly Gly His Ala Leu Arg Val Arg Val Ala						
		1220		1225			1230
	Ala Val Asp Gly Gly Ala Val Ser Val Thr Ala Ala Asp His Ala Gly						
10		1235		1240			1245
	Asn Pro Val Leu Ser Ala Arg Ser Leu Ala Leu Arg Arg Ile Thr Ala						
		1250		1255			1260
	Asp Arg Leu Pro Ala Ala Pro Val Ala Pro Leu Tyr Arg Val Asp Trp						
15		1265		1270		1275	1280
	Leu Pro Phe Pro Gly Pro Val Pro Val Ser Ala Gly Gly Arg Trp Ala						
		1285		1290			1295
20	Val Val Gly Pro Glu Ala Glu Ala Thr Ala Ala Gly Leu Arg Ala Val						
		1300		1305			1310
	Gly Leu Asp Val Arg Thr His Ala Leu Pro Leu Gly Glu Pro Leu Pro						
		1315		1320			1325
25	Pro Gln Ala Gly Thr Asp Ala Glu Val Ile Ile Leu Asp Leu Thr Thr						
		1330		1335			1340
	Thr Ala Ala Gly Arg Thr Ala Ser Asp Gly Gly Arg Leu Ser Leu Leu						
		1345		1350		1355	1360
30	Asp Glu Val Arg Ala Thr Val Arg Arg Thr Leu Glu Ala Val Gln Ala						
		1365		1370			1375
	Arg Leu Ala Asp Thr Glu Thr Ala Pro Asp Val Asp Val Arg Thr Ala						
35		1380		1385			1390
	Ala Arg Pro Arg Thr Ala Ala Arg Thr Ser Pro Arg Val Asp Thr Arg						
		1395		1400			1405
	Thr Gly Ala Arg Thr Ala Asp Gly Pro Arg Leu Val Val Leu Thr Arg						
40		1410		1415			1420
	Gly Ala Ala Gly Pro Glu Gly Gly Ala Ala Asp Pro Ala Gly Ala Ala						
		1425		1430		1435	1440
45	Val Trp Gly Leu Val Arg Val Ala Gln Ala Glu Gln Pro Gly Arg Phe						
		1445		1450			1455
	Thr Leu Val Asp Val Asp Gly Thr Gln Ala Ser Leu Arg Ala Leu Pro						
		1460		1465			1470
50	Gly Leu Leu Ala Thr Asp Ala Gly Gln Ser Ala Val Arg Asp Gly Arg						
		1475		1480			1485
	Val Thr Val Pro Arg Leu Val Pro Val Ala Asp Pro Val Pro His Gly						
		1490		1495			1500
55	Gly Gly Thr Ala Ala Asp Gly Thr Gly Ala Gly Glu Pro Ser Ala Thr						
		1505		1510		1515	1520

EP 0 791 655 A2

5 Leu Asp Pro Glu Gly Thr Val Leu Ile Thr Gly Gly Thr Gly Ala Leu
 1525 1530 1535
 Ala Ala Glu Thr Ala Arg His Leu Val Asp Arg His Lys Val Arg His
 1540 1545 1550
 10 Leu Leu Leu Val Gly Arg Arg Gly Pro Asp Ala Pro Gly Val Asp Arg
 1555 1560 1565
 Leu Val Ala Glu Leu Thr Glu Ser Gly Ala Glu Val Ala Val Arg Ala
 1570 1575 1580
 15 Cys Asp Val Thr Asp Arg Asp Ala Leu Arg Arg Leu Leu Asp Ala Leu
 1585 1590 1595 1600
 Pro Asp Glu His Pro Leu Thr Cys Val Val His Thr Ala Gly Val Leu
 1605 1610 1615
 20 Asp Asp Gly Val Leu Ser Ala Gln Thr Ala Glu Arg Ile Asp Thr Val
 1620 1625 1630
 Leu Arg Pro Lys Ala Asp Ala Ala Val His Leu Asp Glu Leu Thr Arg
 1635 1640 1645
 25 Glu Ile Gly Arg Val Pro Leu Val Leu Tyr Ser Ser Val Ser Ala Thr
 1650 1655 1660
 Leu Gly Ser Ala Gly Gln Ala Gly Tyr Ala Ala Ala Asn Ala Phe Met
 1665 1670 1675 1680
 30 Asp Ala Leu Ala Ala Arg Arg Cys Ala Ala Gly His Pro Ala Leu Ser
 1685 1690 1695
 Leu Gly Trp Gly Trp Trp Ser Gly Val Gly Leu Ala Thr Gly Leu Asp
 1700 1705 1710
 35 Gly Ala Asp Ala Ala Arg Val Arg Arg Ser Gly Leu Ala Pro Leu Asp
 1715 1720 1725
 Ala Gly Ala Ala Leu Asp Leu Leu Asp Arg Ala Leu Thr Arg Pro Glu
 1730 1735 1740
 40 Pro Ala Leu Leu Pro Val Arg Leu Asp Leu Arg Ala Ala Ala Gly Ala
 1745 1750 1755 1760
 Thr Ala Leu Pro Glu Val Leu Arg Asp Leu Ala Gly Val Pro Ala Asp
 1765 1770 1775
 45 Ala Arg Ser Thr Pro Gly Ala Ala Ala Gly Thr Gly Asp Glu Asp Gly
 1780 1785 1790
 50 Ala Val Arg Pro Ala Pro Ala Pro Ala Asp Ala Ala Gly Thr Leu Ala
 1795 1800 1805
 Ala Arg Leu Ala Gly Arg Ser Ala Pro Glu Arg Thr Ala Leu Leu Leu
 1810 1815 1820
 55 Asp Leu Val Arg Thr Glu Val Ala Ala Val Leu Gly His Gly Asp Pro
 1825 1830 1835 1840

EP 0 791 655 A2

Ala Ala Ile Gly Ala Ala Arg Thr Phe Lys Asp Ala Gly Phe Asp Ser
1845 1850 1855

5 Leu Thr Ala Val Asp Leu Arg Asn Arg Leu Asn Thr Arg Thr Gly Leu
1860 1865 1870

Arg Leu Pro Ala Thr Leu Val Phe Asp His Pro Thr Pro Leu Ala Leu
1875 1880 1885

10 Ala Glu Leu Leu Leu Asp Gly Leu Glu Ala Ala Gly Pro Ala Glu Pro
1890 1895 1900

Ala Ala Glu Val Pro Asp Glu Ala Ala Gly Ala Glu Thr Leu Ser Gly
1905 1910 1915 1920

15 Val Ile Asp Arg Leu Glu Arg Ser Leu Ala Ala Thr Asp Asp Gly Asp
1925 1930 1935

Ala Arg Val Arg Ala Ala Arg Arg Leu Arg Gly Leu Leu Asp Ala Leu
1940 1945 1950

20 Pro Ala Gly Pro Gly Ala Ala Ser Gly Pro Asp Ala Gly Glu His Ala
1955 1960 1965

Pro Gly Arg Gly Asp Val Val Ile Asp Arg Leu Arg Ser Ala Ser Asp
1970 1975 1980

25 Asp Asp Leu Phe Asp Leu Leu Asp Ser Asp Phe Gln
1985 1990 1995

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3724 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Ser Ala Thr Asn Glu Glu Lys Leu Arg Glu Tyr Leu Arg Arg Ala
1 5 10 15

Met Ala Asp Leu His Ser Ala Arg Glu Arg Leu Arg Glu Val Glu Ser
20 25 30

Ala Ser Arg Glu Pro Ile Ala Ile Val Gly Met Ala Cys Arg Tyr Pro
35 40 45

Gly Gly Val Ala Ser Pro Glu Glu Leu Trp Asp Leu Val Ala Ala Gly
50 55 60

Thr Asp Ala Ile Ser Pro Phe Pro Val Asp Arg Gly Trp Asp Ala Glu
65 70 75 80

55 Gly Leu Tyr Asp Pro Glu Pro Gly Val Pro Gly Lys Ser Tyr Val Arg
85 90 95

EP 0 791 655 A2

	Glu Gly Gly Phe Leu His Ser Ala Ala Glu Phe Asp Ala Glu Phe Phe	
	100 105 110	
5	Gly Ile Ser Pro Arg Glu Ala Ala Met Asp Pro Gln Gln Arg Leu	
	115 120 125	
	Leu Leu Glu Thr Ser Trp Glu Ala Leu Glu Arg Ala Gly Ile Val Pro	
	130 135 140	
10	Ala Ser Leu Arg Gly Thr Arg Thr Gly Val Phe Thr Gly Val Met Tyr	
	145 150 155 160	
	His Asp Tyr Gly Ser His Gln Val Gly Thr Ala Ala Asp Pro Ser Gly	
	165 170 175	
15	Gln Leu Gly Leu Gly Thr Ala Gly Ser Val Ala Ser Gly Arg Val Ala	
	180 185 190	
	Tyr Thr Leu Gly Leu Gln Gly Pro Ala Val Thr Met Asp Thr Ala Cys	
	195 200 205	
20	Ser Ser Ser Leu Val Ala Leu His Leu Ala Val Gln Ser Leu Arg Arg	
	210 215 220	
	Gly Glu Cys Asp Leu Ala Leu Ala Gly Gly Ala Thr Val Leu Ala Thr	
25	225 230 235 240	
	Pro Thr Val Phe Val Glu Phe Ser Arg Gln Arg Gly Leu Ala Ala Asp	
	245 250 255	
30	Gly Arg Cys Lys Ala Phe Ala Glu Gly Ala Asp Gly Thr Ala Trp Ala	
	260 265 270	
	Glu Gly Ala Gly Val Leu Leu Val Glu Arg Leu Ser Asp Ala Arg Arg	
	275 280 285	
35	Asn Gly His Arg Val Leu Ala Val Val Arg Gly Ser Ala Val Asn Gln	
	290 295 300	
	Asp Gly Ala Ser Asn Gly Leu Thr Ala Pro Ser Gly Pro Ala Gln Gln	
	305 310 315 320	
40	Arg Val Ile Arg Asp Ala Leu Ala Asp Ala Gly Leu Thr Pro Ala Asp	
	325 330 335	
	Val Asp Ala Val Glu Ala His Gly Thr Gly Thr Pro Leu Gly Asp Pro	
	340 345 350	
45	Ile Glu Ala Gly Ala Leu Met Ala Thr Tyr Gly Ser Glu Arg Val Gly	
	355 360 365	
	Asp Pro Leu Trp Leu Gly Ser Leu Lys Ser Asn Ile Gly His Thr Gln	
	370 375 380	
50	Ala Ala Ala Gly Ala Ala Gly Val Ile Lys Met Val Gln Ala Leu Arg	
	385 390 395 400	
	Gln Ser Glu Leu Pro Arg Thr Leu His Val Asp Ala Pro Ser Ala Lys	
55	405 410 415	

EP 0 791 655 A2

Val Glu Trp Asp Ala Gly Ala Val Gln Leu Leu Thr Gly Val Arg Pro
420 425 430

5 Trp Pro Arg Arg Glu His Arg Pro Arg Arg Ala Ala Val Ser Ala Phe
435 440 445

Gly Val Ser Gly Thr Asn Ala His Val Ile Ile Glu Glu Pro Pro Ala
450 455 460

10 Ala Gly Asp Thr Ser Pro Ala Gly Asp Thr Pro Glu Pro Gly Glu Ala
465 470 475 480

Thr Ala Ser Pro Ser Thr Ala Ala Gly Pro Ser Ser Pro Ser Ala Val
485 490 495

15 Ala Gly Pro Leu Ser Pro Ser Ser Pro Ala Val Val Trp Pro Leu Ser
500 505 510

Ala Glu Thr Ala Pro Ala Leu Arg Ala Gln Ala Ala Arg Leu Arg Ala
515 520 525

20 His Leu Glu Arg Leu Pro Gly Thr Ser Pro Thr Asp Ile Gly His Ala
530 535 540

Leu Ala Ala Glu Arg Ala Ala Leu Thr Arg Arg Val Val Leu Leu Gly
545 550 555 560

25 Asp Asp Gly Ala Pro Val Asp Ala Leu Ala Ala Leu Ala Ala Gly Glu
565 570 575

Thr Thr Pro Asp Ala Val His Gly Thr Ala Ala Asp Ile Arg Arg Val
580 585 590

30 Ala Phe Val Phe Pro Gly Gln Gly Ser Gln Trp Ala Gly Met Gly Ala
595 600 605

Glu Leu Leu Asp Thr Ala Pro Ala Phe Ala Ala Glu Leu Asp Arg Cys
610 615 620

35 Gln Gly Ala Leu Ser Pro Tyr Val Asp Trp Asn Leu Ala Asp Val Leu
625 630 635 640

Arg Gly Ala Pro Ala Ala Pro Gly Leu Asp Arg Val Asp Val Val Gln
645 650 655

40 Pro Ala Thr Phe Ala Val Met Val Gly Leu Ala Ala Leu Trp Arg Ser
660 665 670

45 Leu Gly Val Glu Pro Ala Ala Val Ile Gly His Ser Gln Gly Glu Ile
675 680 685

Ala Ala Ala Cys Val Ala Gly Ala Leu Ser Leu Glu Asp Ala Ala Arg
690 695 700

50 Ile Val Ala Leu Arg Ser Gln Val Ile Ala Arg Glu Leu Ala Gly Arg
705 710 715 720

Gly Gly Met Ala Ser Val Ala Leu Pro Ala Ala Glu Val Glu Ala Arg
725 730 735

55 Leu Ala Gly Gly Val Glu Ile Ala Ala Val Asn Gly Pro Gly Ser Thr

EP 0 791 655 A2

	740	745	750
5	Val Val Cys Gly Glu Pro Gly Ala Leu Glu Ala Leu Leu Val Thr Leu 755 760 765		
	Glu Ser Glu Gly Thr Arg Val Arg Arg Ile Asp Val Asp Tyr Ala Ser 770 775 780		
10	His Ser His Tyr Val Glu Ser Ile Arg Ala Glu Leu Ala Thr Val Leu 785 790 795 800		
	Gly Pro Val Arg Pro Arg Arg Gly Asp Val Pro Phe Tyr Ser Thr Val 805 810 815		
15	Glu Ala Ala Leu Leu Asp Thr Ala Thr Leu Asp Ala Asp Tyr Trp Tyr 820 825 830		
	Arg Asn Leu Arg Leu Pro Val Arg Phe Glu Pro Thr Val Arg Ala Met 835 840 845		
20	Leu Asp Asp Gly Val Asp Ala Phe Val Glu Cys Ser Ala His Pro Val 850 855 860		
	Leu Thr Val Gly Val Arg Gln Thr Val Glu Ser Ala Gly Gly Ala Val 865 870 875 880		
25	Pro Ala Leu Ala Ser Leu Arg Arg Asp Glu Gly Gly Leu Arg Arg Phe 885 890 895		
	Leu Thr Ser Ala Ala Glu Ala Gln Val Val Gly Val Pro Val Asp Trp 900 905 910		
30	Ala Thr Leu Arg Pro Gly Ala Gly Arg Val Asp Leu Pro Thr Tyr Ala 915 920 925		
	Phe Gln Arg Glu Arg His Trp Val Gly Pro Ala Arg Pro Asp Ser Ala 930 935 940		
35	Ala Thr Ala Ala Thr Thr Gly Asp Asp Ala Pro Glu Pro Gly Asp Arg 945 950 955 960		
	Leu Gly Tyr His Val Ala Trp Lys Gly Leu Arg Ser Thr Thr Gly Gly 965 970 975		
40	Trp Arg Pro Gly Leu Arg Leu Leu Ile Val Pro Thr Gly Asp Gln Tyr 980 985 990		
	Thr Ala Leu Ala Asp Thr Leu Glu Gln Ala Val Ala Ser Phe Gly Gly 995 1000 1005		
45	Thr Val Arg Arg Val Ala Phe Asp Pro Ala Arg Thr Gly Arg Ala Glu 1010 1015 1020		
	Leu Phe Gly Leu Leu Glu Thr Glu Ile Asn Gly Asp Thr Ala Val Thr 1025 1030 1035 1040		
50	Gly Val Val Ser Leu Leu Gly Leu Cys Thr Asp Gly Arg Pro Asp His 1045 1050 1055		
55	Pro Ala Val Pro Val Ala Val Thr Ala Thr Leu Ala Leu Val Gln Ala 1060 1065 1070		

Leu Ala Asp Leu Gly Ser Thr Ala Pro Leu Trp Thr Val Thr Cys Gly
 1075 1080 1085
 5 Ala Val Ala Thr Ala Pro Asp Glu Leu Pro Cys Thr Ala Gly Ala Gln
 1090 1095 1100
 Leu Trp Gly Leu Gly Arg Val Ala Ala Leu Glu Leu Pro Glu Val Trp
 1105 1110 1115 1120
 10 Gly Gly Leu Ile Asp Leu Pro Ala Arg Pro Asp Ala Arg Val Leu Asp
 1125 1130 1135
 Arg Leu Ala Gly Val Leu Ala Glu Pro Gly Gly Glu Asp Gln Ile Ala
 1140 1145 1150
 15 Val Arg Met Ala Gly Val Phe Gly Arg Arg Val Leu Arg Asn Pro Ala
 1155 1160 1165
 Asp Ser Arg Pro Pro Ala Trp Arg Ala Arg Gly Thr Val Leu Ile Ala
 1170 1175 1180
 20 Gly Asp Leu Thr Thr Val Pro Gly Arg Leu Val Arg Ser Leu Leu Glu
 1185 1190 1195 1200
 Asp Gly Ala Asp Arg Val Val Leu Ala Gly Pro Asp Ala Pro Ala Gln
 1205 1210 1215
 25 Ala Ala Ala Ala Gly Leu Thr Gly Val Ser Leu Val Pro Val Arg Cys
 1220 1225 1230
 Asp Val Thr Asp Arg Ala Ala Leu Ala Ala Leu Leu Asp Glu His Ala
 1235 1240 1245
 30 Pro Thr Val Ala Val His Ala Pro Pro Leu Val Pro Leu Ala Pro Leu
 1250 1255 1260
 Arg Glu Thr Ala Pro Gly Asp Ile Ala Ala Ala Leu Ala Ala Lys Thr
 1265 1270 1275 1280
 35 Thr Ala Ala Gly His Leu Val Asp Leu Ala Pro Ala Ala Gly Leu Asp
 1285 1290 1295
 40 Ala Leu Val Leu Phe Ser Ser Val Ser Gly Val Trp Gly Gly Ala Ala
 1300 1305 1310
 Gln Gly Gly Tyr Ala Ala Ala Ser Ala His Leu Asp Ala Leu Ala Glu
 1315 1320 1325
 45 Arg Ala Arg Ala Ala Gly Val Pro Ala Phe Ser Val Ala Trp Ser Pro
 1330 1335 1340
 Trp Ala Gly Gly Thr Pro Ala Asp Gly Ala Glu Ala Glu Phe Leu Ser
 1345 1350 1355 1360
 50 Arg Arg Gly Leu Ala Pro Leu Asp Pro Asp Gln Ala Val Arg Thr Leu
 1365 1370 1375
 Arg Arg Met Leu Glu Arg Gly Ser Ala Cys Gly Ala Val Ala Asp Val
 1380 1385 1390
 55

EP 0 791 655 A2

	Glu Trp Ser Arg Phe Ala Ala Ser Tyr Thr Trp Val Arg Pro Ala Val	
	1395	1400 1405
5	Leu Phe Asp Asp Ile Pro Asp Val Gln Arg Leu Arg Ala Ala Glu Leu	
	1410	1415 1420
	Ala Pro Ser Thr Gly Asp Ser Thr Thr Ser Glu Leu Val Arg Glu Leu	
	1425	1430 1435 1440
10	Thr Ala Gln Ser Gly His Lys Arg His Ala Thr Leu Leu Arg Leu Val	
		1445 1450 1455
	Arg Ala His Ala Ala Ala Val Leu Gly Gln Ser Ser Gly Asp Ala Val	
		1460 1465 1470
15	Ser Ser Ala Arg Ala Phe Arg Asp Leu Gly Phe Asp Ser Leu Thr Ala	
		1475 1480 1485
	Leu Glu Leu Arg Asp Arg Leu Ser Thr Ser Thr Gly Leu Lys Leu Pro	
		1490 1495 1500
20	Thr Ser Leu Val Phe Asp His Ser Ser Pro Ala Ala Leu Ala Arg His	
		1505 1510 1515 1520
	Leu Gly Glu Glu Leu Leu Gly Arg Asn Asp Thr Ala Asp Arg Ala Gly	
		1525 1530 1535
25	Pro Asp Thr Pro Val Arg Thr Asp Glu Pro Ile Ala Ile Ile Gly Met	
		1540 1545 1550
	Ala Cys Arg Leu Pro Gly Gly Val Gln Ser Pro Glu Asp Leu Trp Asp	
		1555 1560 1565
30	Leu Leu Thr Gly Gly Thr Asp Ala Ile Thr Pro Phe Pro Thr Asn Arg	
		1570 1575 1580
	Gly Trp Asp Asn Glu Thr Leu Tyr Asp Pro Asp Pro Asp Ser Pro Gly	
		1585 1590 1595 1600
35	His His Thr Tyr Val Arg Glu Gly Gly Phe Leu His Asp Ala Ala Glu	
		1605 1610 1615
	Phe Asp Pro Gly Phe Phe Gly Ile Ser Pro Arg Glu Ala Leu Ala Met	
		1620 1625 1630
40	Asp Pro Gln Gln Arg Leu Ile Leu Glu Thr Ser Trp Glu Ser Phe Glu	
		1635 1640 1645
45	Arg Ala Gly Ile Asp Pro Val Glu Leu Arg Gly Ser Arg Thr Gly Val	
		1650 1655 1660
	Phe Val Gly Thr Asn Gly Gln His Tyr Val Pro Leu Leu Gln Asp Gly	
		1665 1670 1675 1680
50	Asp Glu Asn Phe Asp Gly Tyr Ile Ala Thr Gly Asn Ser Ala Ser Val	
		1685 1690 1695
	Met Ser Gly Arg Leu Ser Tyr Val Phe Gly Leu Glu Gly Pro Ala Val	
		1700 1705 1710
55	Thr Val Asp Thr Ala Cys Ser Ala Ser Leu Ala Ala Leu His Leu Ala	

EP 0 791 655 A2

	1715	1720	1725
5	Val Gln Ser Leu Arg Arg Gly Glu Cys Asp Tyr Ala Leu Ala Gly Gly 1730 1735 1740		
	Ala Thr Val Met Ser Thr Pro Glu Met Leu Val Glu Phe Ala Arg Gln 1745 1750 1755 1760		
10	Arg Ala Val Ser Pro Asp Gly Arg Ser Lys Ala Phe Ala Glu Ala Ala 1765 1770 1775		
	Asp Gly Val Gly Leu Ala Glu Gly Ala Gly Met Leu Leu Val Glu Arg 1780 1785 1790		
15	Leu Ser Glu Ala Gln Lys Lys Gly His Pro Val Leu Ala Val Val Arg 1795 1800 1805		
	Gly Ser Ala Val Asn Gln Asp Gly Ala Ser Asn Gly Leu Thr Ala Pro 1810 1815 1820		
20	Ser Gly Pro Ala Gln Gln Arg Val Ile Arg Glu Ala Leu Ala Asp Ala 1825 1830 1835 1840		
	Gly Leu Thr Pro Ala Asp Val Asp Ala Val Glu Ala His Gly Thr Gly 1845 1850 1855		
25	Thr Pro Leu Gly Asp Pro Ile Glu Ala Gly Ala Leu Leu Ala Thr Tyr 1860 1865 1870		
	Gly Arg Asp Arg Arg Asp Gly Pro Leu Trp Leu Gly Ser Leu Lys Ser 1875 1880 1885		
30	Asn Ile Gly His Thr Gln Ala Ala Ala Gly Val Ala Gly Val Ile Lys 1890 1895 1900		
	Met Val Leu Ala Leu Arg His Gly Glu Leu Pro Arg Thr Leu His Ala 1905 1910 1915 1920		
35	Ser Thr Ala Ser Ser Arg Ile Asp Trp Asp Ala Gly Ala Val Glu Leu 1925 1930 1935		
	Leu Asp Glu Ala Arg Pro Trp Leu Gln Arg Ala Glu Gly Pro Arg Arg 1940 1945 1950		
40	Ala Gly Ile Ser Ser Phe Gly Ile Ser Gly Thr Asn Ala His Leu Val 1955 1960 1965		
	Ile Glu Glu Pro Pro Glu Pro Thr Ala Pro Glu Leu Leu Ala Pro Glu 1970 1975 1980		
45	Pro Ala Ala Asp Gly Asp Val Trp Ser Glu Glu Trp Trp His Glu Val 1985 1990 1995 2000		
50	Thr Val Pro Leu Met Met Ser Ala His Asn Glu Ala Ala Leu Arg Asp 2005 2010 2015		
	Gln Ala Arg Arg Leu Arg Ala Asp Leu Leu Ala His Pro Glu Leu His 2020 2025 2030		
55	Pro Ala Asp Val Gly Tyr Thr Leu Ile Thr Thr Arg Thr Arg Phe Glu 2035 2040 2045		

EP 0 791 655 A2

Gln Arg Ala Ala Val Val Gly Glu Asn Phe Thr Glu Leu Ile Ala Ala
 2050 2055 2060
 5 Leu Asp Asp Leu Val Glu Gly Arg Pro His Pro Leu Val Leu Arg Gly
 2065 2070 2075 2080
 Thr Ala Gly Thr Ser Asp Gln Val Val Phe Val Phe Pro Gly Gln Gly
 2085 2090 2095
 10 Ser Gln Trp Pro Glu Met Ala Asp Gly Leu Leu Ala Arg Ser Ser Gly
 2100 2105 2110
 Ser Gly Ser Phe Leu Glu Thr Ala Arg Ala Cys Asp Leu Ala Leu Arg
 2115 2120 2125
 15 Pro His Leu Gly Trp Ser Val Leu Asp Val Leu Arg Arg Glu Pro Gly
 2130 2135 2140
 Ala Pro Ser Leu Asp Arg Val Asp Val Val Gln Pro Val Leu Phe Thr
 2145 2150 2155 2160
 20 Met Met Val Ser Leu Ala Glu Thr Trp Arg Ser Leu Gly Val Glu Pro
 2165 2170 2175
 Ala Ala Val Val Gly His Ser Gln Gly Glu Ile Ala Ala Ala Tyr Val
 2180 2185 2190
 25 Ala Gly Ala Leu Thr Leu Asp Asp Ala Ala Arg Ile Val Ala Leu Arg
 2195 2200 2205
 30 Ser Gln Ala Trp Leu Arg Leu Ala Gly Lys Gly Gly Met Val Ala Val
 2210 2215 2220
 Thr Leu Ser Glu Arg Asp Leu Arg Pro Arg Leu Glu Pro Trp Ser Asp
 2225 2230 2235 2240
 35 Arg Leu Ala Val Ala Ala Val Asn Gly Pro Glu Thr Cys Ala Val Ser
 2245 2250 2255
 Gly Asp Pro Asp Ala Leu Ala Glu Leu Val Ala Glu Leu Gly Ala Glu
 2260 2265 2270
 40 Gly Val His Ala Arg Pro Ile Pro Gly Val Asp Thr Ala Gly His Ser
 2275 2280 2285
 Pro Gln Val Asp Thr Leu Glu Ala His Leu Arg Lys Val Leu Ala Pro
 2290 2295 2300
 45 Val Ala Pro Arg Thr Ser Asp Ile Pro Phe Tyr Ser Thr Val Thr Gly
 2305 2310 2315 2320
 Gly Leu Ile Asp Thr Ala Glu Leu Asp Ala Asp Tyr Trp Tyr Arg Asn
 2325 2330 2335
 50 Met Arg Glu Pro Val Glu Phe Glu Gln Ala Thr Arg Ala Leu Ile Ala
 2340 2345 2350
 Asp Gly His Asp Val Phe Leu Glu Ser Ser Pro His Pro Met Leu Ala
 2355 2360 2365
 55

EP 0 791 655 A2

	Val Ser Leu Gln Glu Thr Ile Ser Asp Ala Gly Ser Pro Ala Ala Val	
	2370	2375 2380
5	Leu Gly Thr Leu Arg Arg Gly Gln Gly Gly Pro Arg Trp Leu Gly Val	
	2385	2390 2395 2400
	Ala Leu Cys Arg Ala Tyr Thr His Gly Leu Glu Ile Asp Ala Glu Ala	
		2405 2410 2415
10	Ile Phe Gly Pro Asp Ser Arg Gln Val Glu Leu Pro Thr Tyr Pro Phe	
		2420 2425 2430
	Gln Arg Glu Arg Tyr Trp Tyr Ser Pro Gly His Arg Gly Asp Asp Pro	
		2435 2440 2445
15	Ala Ser Leu Gly Leu Asp Ala Val Asp His Pro Leu Leu Gly Ser Gly	
		2450 2455 2460
	Val Glu Leu Pro Glu Ser Gly Asp Arg Met Tyr Thr Ala Arg Leu Gly	
		2465 2470 2475 2480
20	Ala Asp Thr Thr Pro Trp Leu Ala Asp His Ala Leu Leu Gly Ser Pro	
		2485 2490 2495
	Leu Leu Pro Gly Ala Ala Phe Ala Asp Leu Ala Leu Trp Ala Gly Arg	
		2500 2505 2510
25	Gln Ala Gly Thr Gly Arg Val Glu Glu Leu Thr Leu Ala Ala Pro Leu	
		2515 2520 2525
	Val Leu Pro Gly Ser Gly Gly Val Arg Leu Arg Leu Asn Val Gly Ala	
		2530 2535 2540
30	Pro Gly Thr Asp Asp Ala Arg Arg Phe Ala Val His Ala Arg Ala Glu	
		2545 2550 2555 2560
	Gly Ala Thr Asp Trp Thr Leu His Ala Glu Gly Leu Leu Thr Ala Gln	
		2565 2570 2575
35	Asp Thr Ala Asp Ala Pro Asp Ala Ser Ala Ala Thr Pro Pro Pro Gly	
		2580 2585 2590
	Ala Glu Gln Leu Asp Ile Gly Asp Phe Tyr Gln Arg Phe Ser Glu Leu	
		2595 2600 2605
40	Gly Tyr Gly Tyr Gly Pro Phe Phe Arg Gly Leu Val Ser Ala His Arg	
		2610 2615 2620
	Cys Gly Pro Asp Ile His Ala Glu Val Ala Leu Pro Val Gln Ala Gln	
		2625 2630 2635 2640
45	Gly Asp Ala Ala Arg Phe Gly Ile His Pro Ala Leu Leu Asp Ala Ala	
		2645 2650 2655
50	Leu Gln Thr Met Ser Leu Gly Gly Phe Phe Pro Glu Asp Gly Arg Val	
		2660 2665 2670
	Arg Met Pro Phe Ala Leu Arg Gly Val Arg Leu Tyr Arg Ala Gly Ala	
		2675 2680 2685
55	Asp Arg Leu His Val Arg Val Ser Pro Val Ser Glu Asp Ala Val Arg	

EP 0 791 655 A2

	2690	2695	2700
5	Ile Arg Cys Ala Asp Gly Glu Gly Arg Pro Val Ala Glu Ile Glu Ser 2705 2710 2715 2720		
	Phe Ile Met Arg Pro Val Asp Pro Gly Gln Leu Leu Gly Gly Arg Pro 2725 2730 2735		
10	Val Gly Ala Asp Ala Leu Phe Arg Ile Ala Trp Arg Glu Leu Ala Ala 2740 2745 2750		
	Gly Pro Gly Thr Arg Thr Gly Asp Gly Thr Pro Pro Pro Val Arg Trp 2755 2760 2765		
15	Val Leu Ala Gly Pro Asp Ala Leu Gly Leu Ala Glu Ala Ala Asp Ala 2770 2775 2780		
	His Leu Pro Ala Val Pro Gly Pro Asp Gly Ala Leu Pro Ser Pro Thr 2785 2790 2795 2800		
20	Gly Arg Pro Ala Pro Asp Ala Val Val Phe Ala Val Arg Ala Gly Thr 2805 2810 2815		
	Gly Asp Val Ala Ala Asp Ala His Thr Val Ala Cys Arg Val Leu Asp 2820 2825 2830		
25	Leu Val Gln Arg Arg Leu Ala Ala Pro Glu Gly Pro Asp Gly Ala Arg 2835 2840 2845		
	Leu Val Val Ala Thr Arg Gly Ala Val Ala Val Arg Asp Asp Ala Glu 2850 2855 2860		
30	Val Asp Asp Pro Ala Ala Ala Ala Trp Gly Leu Leu Arg Ser Ala 2865 2870 2875 2880		
	Gln Ala Glu Glu Pro Gly Arg Phe Leu Leu Val Asp Leu Asp Asp Asp 2885 2890 2895		
35	Pro Ala Ser Ala Arg Ala Leu Thr Asp Ala Leu Ala Ser Gly Glu Pro 2900 2905 2910		
	Gln Thr Ala Val Arg Ala Gly Thr Val Tyr Val Pro Arg Leu Glu Arg 2915 2920 2925		
40	Ala Ala Asp Arg Thr Asp Gly Pro Leu Thr Pro Pro Asp Asp Gly Ala 2930 2935 2940		
	Trp Arg Leu Gly Arg Gly Thr Asp Leu Thr Leu Asp Gly Leu Ala Leu 2945 2950 2955 2960		
45	Val Pro Ala Pro Asp Ala Glu Ala Pro Leu Glu Pro Gly Gln Val Arg 2965 2970 2975		
	Val Ala Val Arg Ala Ala Gly Val Asn Phe Arg Asp Ala Leu Ile Ala 2980 2985 2990		
50	Leu Gly Met Tyr Pro Gly Glu Ala Glu Met Gly Thr Glu Gly Ala Gly 2995 3000 3005		
	Thr Val Val Glu Val Gly Pro Gly Val Thr Gly Val Ala Val Gly Asp 3010 3015 3020		
55			

EP 0 791 655 A2

Arg Val Leu Gly Leu Trp Asp Gly Gly Leu Gly Pro Leu Cys Val Ala
3025 3030 3035 3040

5 Asp His Arg Leu Leu Ala Pro Val Pro Asp Gly Trp Ser Tyr Ala Gln
3045 3050 3055

Ala Ala Ser Val Pro Ala Val Phe Leu Ser Ala Tyr Tyr Gly Leu Val
3060 3065 3070

10 Thr Leu Ala Gly Leu Arg Pro Gly Glu Arg Val Leu Val His Ala Ala
3075 3080 3085

Ala Gly Gly Val Gly Met Ala Ala Val Gln Ile Ala Arg His Leu Gly
3090 3095 3100

15 Ala Glu Val Leu Ala Thr Ala Ser Pro Gly Lys Trp Asp Ala Leu Arg
3105 3110 3115 3120

Ala Met Gly Ile Thr Asp Asp His Leu Ala Ser Ser Arg Thr Leu Asp
20 3125 3130 3135

Phe Ala Thr Ala Phe Thr Gly Ala Asp Gly Thr Ser Arg Ala Asp Val
3140 3145 3150

25 Val Leu Asn Ser Leu Thr Lys Glu Phe Val Asp Ala Ser Leu Gly Leu
3155 3160 3165

Leu Arg Pro Gly Gly Arg Phe Leu Glu Leu Gly Lys Thr Asp Val Arg
3170 3175 3180

30 Asp Pro Glu Arg Ile Ala Ala Glu His Pro Gly Val Arg Tyr Arg Ala
3185 3190 3195 3200

Phe Asp Leu Asn Glu Ala Gly Pro Asp Ala Leu Gly Arg Leu Leu Arg
3205 3210 3215

35 Glu Leu Met Asp Leu Phe Ala Ala Gly Val Leu His Pro Leu Pro Val
3220 3225 3230

Val Thr His Asp Val Arg Arg Ala Ala Asp Ala Leu Arg Thr Ile Ser
40 3235 3240 3245

Gln Ala Arg His Thr Gly Lys Leu Val Leu Thr Met Pro Pro Ala Trp
3250 3255 3260

His Pro Tyr Gly Thr Val Leu Val Thr Gly Gly Thr Gly Ala Leu Gly
45 3265 3270 3275 3280

Ser Arg Ile Ala Arg His Leu Ala Ser Arg His Gly Val Arg Arg Leu
3285 3290 3295

Leu Ile Ala Ala Arg Arg Gly Pro Asp Gly Glu Gly Ala Ala Glu Leu
50 3300 3305 3310

Val Ala Asp Leu Ala Ala Leu Gly Ala Ser Ala Thr Val Val Ala Cys
3315 3320 3325

55 Asp Val Ser Asp Ala Asp Ala Val Arg Gly Leu Leu Ala Gly Ile Pro
3330 3335 3340

EP 0 791 655 A2

Ala Asp His Pro Leu Thr Ala Val Val His Ser Thr Gly Val Leu Asp
3345 3350 3355 3360

5 Asp Gly Val Leu Pro Gly Leu Thr Pro Glu Arg Met Arg Arg Val Leu
3365 3370 3375

Arg Pro Lys Val Glu Ala Ala Val His Leu Asp Glu Leu Thr Arg Asp
3380 3385 3390

10 Leu Asp Leu Ser Ala Phe Val Leu Phe Ser Ser Ser Ala Gly Leu Leu
3395 3400 3405

Gly Ser Pro Ala Gln Gly Asn Tyr Ala Ala Ala Asn Ala Thr Leu Asp
3410 3415 3420

15 Ala Leu Ala Ala Arg Arg Arg Ser Leu Gly Leu Pro Ser Val Ser Leu
3425 3430 3435 3440

Ala Trp Gly Leu Trp Ser Asp Thr Ser Arg Met Ala His Ala Leu Asp
3445 3450 3455

20 Gln Glu Ser Leu Gln Arg Arg Phe Ala Arg Ser Gly Phe Pro Pro Leu
3460 3465 3470

Ser Ala Thr Leu Gly Ala Ala Leu Phe Asp Ala Ala Leu Arg Val Asp
3475 3480 3485

25 Glu Ala Val Gln Val Pro Met Arg Phe Asp Pro Ala Ala Leu Arg Ala
3490 3495 3500

Thr Gly Ser Val Pro Ala Leu Leu Ser Asp Leu Val Gly Ser Ala Pro
3505 3510 3515 3520

30 Ala Thr Gly Ser Ala Ala Pro Ala Ser Gly Pro Leu Pro Ala Pro Asp
3525 3530 3535

Ala Gly Thr Val Gly Glu Pro Leu Ala Glu Arg Leu Ala Gly Leu Ser
3540 3545 3550

35 Ala Glu Glu Arg His Asp Arg Leu Leu Gly Leu Val Gly Glu His Val
3555 3560 3565

40 Ala Ala Val Leu Gly His Gly Ser Ala Ala Glu Val Arg Pro Asp Arg
3570 3575 3580

Pro Phe Arg Glu Val Gly Phe Asp Ser Leu Thr Ala Val Glu Leu Arg
3585 3590 3595 3600

45 Asn Arg Met Ala Ala Val Thr Gly Val Arg Leu Pro Ala Thr Leu Val
3605 3610 3615

Phe Asp His Pro Thr Pro Ala Ala Leu Ser Ser His Leu Asp Gly Leu
3620 3625 3630

50 Leu Ala Pro Ala Gln Pro Val Thr Thr Thr Pro Leu Leu Ser Glu Leu
3635 3640 3645

Asp Arg Ile Glu Glu Ala Leu Ala Ala Leu Thr Pro Glu His Leu Ala
3650 3655 3660

55 Glu Leu Ala Pro Ala Pro Asp Asp Arg Ala Glu Val Ala Leu Arg Leu

EP 0 791 655 A2

3665 3670 3675 3680
 Asp Ala Leu Ala Asp Arg Trp Arg Ala Leu His Asp Gly Ala Pro Gly
 3685 3690 3695

Ala Asp Asp Asp Ile Thr Asp Val Leu Ser Ser Ala Asp Asp Asp Glu
 3700 3705 3710

Ile Phe Ala Phe Ile Asp Glu Arg Tyr Gly Thr Ser
 3715 3720

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1580 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Ala Asn Glu Glu Lys Leu Arg Ala Tyr Leu Lys Arg Val Thr Gly
 1 5 10 15
 Glu Leu His Arg Ala Thr Glu Gln Leu Arg Ala Leu Asp Arg Arg Ala
 20 25 30
 His Glu Pro Ile Ala Ile Val Gly Ala Ala Cys Arg Leu Pro Gly Gly
 35 40 45
 Val Glu Ser Pro Asp Asp Leu Trp Glu Leu Leu His Ala Gly Ala Asp
 50 55 60
 Ala Val Gly Pro Ala Pro Ala Asp Arg Gly Trp Asp Val Glu Gly Arg
 65 70 75 80
 Tyr Ser Pro Asp Pro Asp Thr Pro Gly Thr Ser Tyr Cys Arg Glu Gly
 85 90 95
 Gly Phe Val Gln Gly Ala Asp Arg Phe Asp Pro Ala Leu Phe Gly Ile
 100 105 110
 Ser Pro Asn Glu Ala Leu Thr Met Asp Pro Gln Gln Arg Leu Leu Leu
 115 120 125
 Glu Thr Ser Trp Glu Ala Leu Glu Arg Ala Gly Leu Asp Pro Gln Ser
 130 135 140
 Leu Ala Gly Ser Arg Thr Gly Val Phe Ala Gly Ala Trp Glu Ser Gly
 145 150 155 160
 Tyr Gln Lys Gly Val Glu Gly Leu Glu Ala Asp Leu Glu Ala Gln Leu
 165 170 175
 Leu Ala Gly Ile Val Ser Phe Thr Ala Gly Arg Val Ala Tyr Ala Leu
 180 185 190
 Gly Leu Glu Gly Pro Ala Leu Thr Ile Asp Thr Ala Cys Ser Ser Ser

EP 0 791 655 A2

	195	200	205
5	Leu Val Ala Leu His Leu Ala 210	Val Gln Ser Leu Arg Arg Gly Glu Cys 215	
	Asp Leu Ala Leu Ala Gly Gly Ala Thr Val Ile Ala Asp Phe Ala Leu 225	230	235 240
10	Phe Thr Gln Phe Ser Arg Gln Arg Gly Leu Ala Pro Asp Gly Arg Cys 245	250	255
	Lys Ala Phe Gly Glu Thr Ala Asp Gly Phe Gly Pro Ala Glu Gly Ala 260	265	270
15	Gly Met Leu Leu Val Glu Arg Leu Ser Asp Ala Arg Arg Asn Gly His 275	280	285
	Pro Val Leu Ala Val Val Arg Gly Ser Ala Val Asn Gln Asp Gly Ala 290	295	300
20	Ser Asn Gly Leu Thr Ala Pro Ser Gly Pro Ala Gln Gln Arg Val Ile 305	310	315 320
	Arg Glu Ala Leu Ala Asp Ala Gly Leu Thr Pro Ala Asp Val Asp Ala 325	330	335
25	Val Glu Ala His Gly Thr Gly Thr Pro Leu Gly Asp Pro Ile Glu Ala 340	345	350
	Gly Ala Leu Met Ala Thr Tyr Gly His Glu Arg Thr Gly Asp Pro Leu 355	360	365
30	Trp Leu Gly Ser Leu Lys Ser Asn Ile Gly His Thr Gln Ala Ala Ala 370	375	380
	Gly Val Ala Gly Val Ile Lys Met Val Leu Ala Leu Arg His Gly Glu 385	390	395 400
35	Leu Pro Arg Thr Leu His Ala Ser Thr Ala Ser Ser Arg Ile Glu Trp 405	410	415
	Asp Ala Gly Ala Val Glu Leu Leu Asp Glu Ala Arg Pro Trp Pro Arg 420	425	430
40	Arg Ala Glu Gly Pro Arg Arg Ala Gly Ile Ser Ser Phe Gly Ile Ser 435	440	445
	Gly Thr Asn Ala His Leu Val Ile Glu Glu Glu Pro Pro Ala Arg Pro 450	455	460
45	Glu Pro Glu Glu Ala Ala Gln Pro Pro Ala Pro Ala Thr Thr Val Leu 465	470	475 480
50	Pro Leu Ser Ala Ala Gly Ala Arg Ser Leu Arg Glu Gln Ala Arg Arg 485	490	495
	Leu Ala Ala His Leu Ala Gly His Glu Glu Ile Thr Ala Ala Asp Ala 500	505	510
55	Ala Arg Ser Ala Ala Thr Thr Arg Ala Ala Leu Ser His Arg Ala Ser		

EP 0 791 655 A2

		515				520				525				
	Val	Leu	Ala	Asp	Asp	Arg	Arg	Ala	Leu	Ile	Asp	Arg	Leu	Thr
		530					535				540			
5	Ala	Glu	Asp	Arg	Lys	Asp	Pro	Gly	Val	Thr	Val	Gly	Glu	Ala
	545					550					555			560
	Gly	Arg	Pro	Pro	Val	Phe	Val	Phe	Pro	Gly	Gln	Gly	Ser	Gln
					565					570				575
10	Gly	Met	Gly	Ala	Glu	Leu	Leu	Asp	Arg	Ala	Pro	Val	Phe	Arg
				580					585					590
	Ala	Glu	Glu	Cys	Ala	Arg	Ala	Leu	Ala	Ala	His	Leu	Asp	Trp
				595				600					605	
15	Leu	Asp	Val	Leu	Arg	Asp	Ala	Pro	Gly	Ala	Pro	Pro	Ile	Asp
		610					615						620	
	Asp	Val	Val	Gln	Pro	Thr	Leu	Phe	Thr	Met	Met	Val	Ser	Leu
20		625				630					635			640
	Leu	Trp	Glu	Ser	His	Gly	Val	Arg	Pro	Ala	Ala	Val	Val	Gly
					645					650				655
25	Gln	Gly	Glu	Ile	Ala	Ala	Ala	His	Ala	Ala	Gly	Ala	Leu	Ser
				660					665					670
	Asp	Ala	Ala	Arg	Val	Ile	Ala	Glu	Arg	Ser	Arg	Leu	Trp	Lys
				675				680					685	
30	Ala	Gly	Asn	Gly	Gly	Met	Leu	Ser	Val	Met	Ala	Pro	Ala	Asp
						690						700		
	Arg	Glu	Leu	Met	Glu	Pro	Trp	Ala	Glu	Arg	Met	Ser	Val	Ala
		705				710					715			720
35	Asn	Gly	Pro	Ala	Ser	Val	Thr	Val	Ala	Gly	Asp	Ala	Arg	Ala
					725					730				735
	Glu	Phe	Gly	Gly	Arg	Leu	Ser	Ala	Ala	Gly	Val	Leu	Arg	Trp
				740					745					750
40	Ala	Gly	Val	Asp	Phe	Ala	Gly	His	Ser	Pro	Gln	Val	Glu	Gln
				755				760					765	
	Ala	Glu	Leu	Leu	Asp	Thr	Leu	Gly	Thr	Val	Arg	Pro	Thr	Ala
45						770		775				780		
	Leu	Pro	Phe	Phe	Ser	Thr	Val	Thr	Ala	Ala	Ala	His	Glu	Pro
					785						795			800
	Leu	Asp	Ala	Ala	Tyr	Trp	Tyr	Arg	Asn	Met	Arg	Glu	Pro	Val
50					805					810				815
	Ala	Ser	Thr	Leu	Arg	Thr	Leu	Leu	Arg	Glu	Gly	His	Arg	Thr
				820					825					830
55	Glu	Met	Gly	Pro	His	Pro	Leu	Leu	Gly	Ala	Ala	Ile	Asp	Glu
				835				840					845	

EP 0 791 655 A2

	Glu	Ala	Glu	Gly	Val	His	Ala	Thr	Ala	Leu	Ala	Thr	Leu	His	Arg	Gly	
	850						855					860					
5	Ser	Gly	Gly	Leu	Asp	Arg	Phe	Arg	Ser	Ser	Val	Gly	Ala	Ala	Phe	Ala	
	865					870					875					880	
	His	Gly	Val	Arg	Val	Asp	Trp	Asp	Ala	Leu	Phe	Glu	Gly	Ser	Gly	Ala	
					885					890					895		
10	Arg	Arg	Val	Pro	Leu	Pro	Thr	Tyr	Ala	Phe	Ser	Arg	Asp	Arg	Tyr	Trp	
			900						905					910			
	Leu	Pro	Thr	Ala	Ile	Gly	Arg	Arg	Ala	Val	Glu	Ala	Ala	Pro	Val	Asp	
			915					920					925				
15	Ala	Ser	Ala	Pro	Gly	Arg	Tyr	Arg	Val	Thr	Trp	Thr	Pro	Val	Ala	Ser	
	930					935						940					
	Asp	Asp	Ser	Gly	Arg	Pro	Ser	Gly	Arg	Trp	Leu	Leu	Val	Gln	Thr	Pro	
	945					950					955					960	
20	Gly	Thr	Ala	Pro	Asp	Glu	Ala	Asp	Thr	Ala	Ala	Ser	Ala	Leu	Gly	Ala	
					965					970					975		
	Ala	Gly	Val	Val	Val	Glu	Arg	Cys	Leu	Leu	Asp	Pro	Thr	Glu	Ala	Ala	
				980					985					990			
25	Arg	Val	Thr	Leu	Thr	Glu	Arg	Leu	Ala	Glu	Leu	Asp	Ala	Gln	Pro	Glu	
			995					1000					1005				
	Gly	Leu	Ala	Gly	Val	Leu	Val	Leu	Pro	Gly	Arg	Pro	Gln	Ser	Thr	Ala	
30		1010				1015						1020					
	Pro	Ala	Asp	Ala	Ser	Pro	Leu	Asp	Pro	Gly	Thr	Ala	Ala	Val	Leu	Leu	
	1025					1030					1035					1040	
35	Val	Val	Gln	Ala	Val	Pro	Asp	Ala	Ala	Pro	Lys	Ala	Arg	Ile	Trp	Val	
				1045						1050				1055			
	Val	Thr	Arg	Gly	Ala	Val	Ala	Val	Gly	Ser	Gly	Glu	Val	Pro	Cys	Ala	
			1060						1065				1070				
40	Val	Gly	Ala	Arg	Val	Trp	Gly	Leu	Gly	Arg	Val	Ala	Ala	Leu	Glu	Val	
		1075					1080						1085				
	Pro	Val	Gln	Trp	Gly	Gly	Leu	Val	Asp	Val	Ala	Val	Gly	Ala	Gly	Val	
		1090					1095					1100					
45	Arg	Glu	Trp	Arg	Arg	Val	Val	Gly	Val	Val	Ala	Gly	Gly	Gly	Glu	Asp	
	1105					1110					1115					1120	
	Gln	Val	Ala	Val	Arg	Gly	Gly	Gly	Val	Phe	Gly	Arg	Arg	Leu	Val	Gly	
				1125						1130					1135		
50	Val	Gly	Val	Arg	Gly	Gly	Ser	Gly	Val	Trp	Arg	Ala	Arg	Gly	Cys	Val	
			1140						1145					1150			
	Val	Val	Thr	Gly	Gly	Leu	Gly	Gly	Val	Gly	Gly	His	Val	Ala	Arg	Trp	
55			1155					1160					1165				

EP 0 791 655 A2

Leu Ala Arg Ser Gly Ala Glu His Val Val Leu Ala Gly Arg Arg Gly
1170 1175 1180

5 Gly Gly Val Val Gly Ala Val Glu Leu Glu Arg Glu Leu Val Gly Leu
1185 1190 1195 1200

Gly Ala Lys Val Thr Phe Val Ser Cys Asp Val Gly Asp Arg Ala Ser
1205 1210 1215

10 Met Val Gly Leu Leu Gly Val Val Glu Gly Leu Gly Val Pro Leu Arg
1220 1225 1230
Gly Val Phe His Ala Ala Gly Val Ala Gln Val Ser Gly Leu Gly Glu
1235 1240 1245

15 Val Ser Leu Ala Glu Ala Gly Gly Val Leu Gly Gly Lys Ala Val Gly
1250 1255 1260

Ala Glu Leu Leu Asp Glu Leu Thr Ala Gly Val Glu Leu Asp Ala Phe
1265 1270 1275 1280

20 Val Leu Phe Ser Ser Gly Ala Gly Val Trp Gly Ser Gly Gly Gln Ser
1285 1290 1295

Val Tyr Ala Ala Ala Asn Ala His Leu Asp Ala Leu Ala Glu Arg Arg
1300 1305 1310

25 Arg Ala Gln Gly Arg Pro Ala Thr Ser Val Ala Trp Gly Leu Trp Gly
1315 1320 1325

Gly Glu Gly Met Gly Ala Asp Glu Gly Val Thr Glu Phe Tyr Ala Glu
1330 1335 1340

30 Arg Gly Leu Ala Pro Met Arg Pro Glu Ser Gly Ile Glu Ala Leu His
1345 1350 1355 1360

Thr Ala Leu Asn Glu Gly Asp Thr Cys Val Thr Val Ala Asp Ile Asp
1365 1370 1375

35 Trp Glu His Phe Val Thr Gly Phe Thr Ala Tyr Arg Pro Ser Pro Leu
1380 1385 1390

Ile Ser Asp Ile Pro Gln Val Arg Ala Leu Arg Thr Pro Glu Pro Thr
1395 1400 1405

40 Val Asp Ala Ser Asp Gly Leu Arg Arg Arg Val Asp Ala Ala Leu Thr
1410 1415 1420

Pro Arg Glu Arg Thr Lys Val Leu Val Asp Leu Val Arg Thr Val Ala
1425 1430 1435 1440

Ala Glu Val Leu Gly His Asp Gly Ile Gly Gly Ile Gly His Asp Val
1445 1450 1455

50 Ala Phe Arg Asp Leu Gly Phe Asp Ser Leu Ala Ala Val Arg Met Arg
1460 1465 1470

Gly Arg Leu Ala Glu Ala Thr Gly Leu Val Leu Pro Ala Thr Val Ile
1475 1480 1485

55 Phe Asp His Pro Thr Val Asp Arg Leu Gly Gly Ala Leu Leu Glu Arg

EP 0 791 655 A2

	1490	1495	1500
5	Leu Ser Ala Asp Glu Pro Ala Pro Gly Gly Ala Pro Glu Pro Ala Gly 1505	1510	1515 1520
	Gly Arg Pro Ala Thr Pro Pro Pro Ala Pro Glu Pro Ala Val His Asp 1525	1530	1535
10	Ala Asp Ile Asp Glu Leu Asp Ala Asp Ala Leu Ile Arg Leu Ala Thr 1540	1545	1550
	Gly Thr Ala Gly Pro Ala Asp Gly Thr Pro Ala Asp Gly Gly Pro Asp 1555	1560	1565
15	Ala Ala Ala Thr Ala Pro Asp Gly Ala Pro Glu Gln 1570	1575	1580

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1891 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

30	Met Ser Pro Ser Met Asp Glu Val Leu Gly Ala Leu Arg Thr Ser Val 1 5 10 15
	Lys Glu Thr Glu Arg Leu Arg Arg His Asn Arg Glu Leu Leu Ala Gly 20 25 30
35	Ala His Glu Pro Val Ala Ile Val Gly Met Ala Cys Arg Tyr Pro Gly 35 40 45
	Gly Val Ser Thr Pro Asp Asp Leu Trp Glu Leu Ala Ala Asp Gly Val 50 55 60
40	Asp Ala Ile Thr Pro Phe Pro Ala Asp Arg Gly Trp Asp Glu Asp Ala 65 70 75 80
	Val Tyr Ser Pro Asp Pro Asp Thr Pro Gly Thr Thr Tyr Cys Arg Glu 85 90 95
45	Gly Gly Phe Leu Thr Gly Ala Gly Asp Phe Asp Ala Ala Phe Phe Gly 100 105 110
	Ile Ser Pro Asn Glu Ala Leu Val Met Asp Pro Gln Gln Arg Leu Leu 115 120 125
50	Leu Glu Thr Ser Trp Glu Thr Leu Glu Arg Ala Gly Ile Val Pro Ala 130 135 140
55	Ser Leu Arg Gly Ser Arg Thr Gly Val Phe Val Gly Ala Ala His Thr 145 150 155 160

EP 0 791 655 A2

	Gly	Tyr	Val	Thr	Asp	Thr	Ala	Arg	Ala	Pro	Glu	Gly	Thr	Glu	Gly	Tyr	
					165					170					175		
5	Leu	Leu	Thr	Gly	Asn	Ala	Asp	Ala	Val	Met	Ser	Gly	Arg	Ile	Ala	Tyr	
				180					185					190			
	Ser	Leu	Gly	Leu	Glu	Gly	Pro	Ala	Leu	Thr	Ile	Gly	Thr	Ala	Cys	Ser	
			195					200					205				
10	Ser	Ser	Leu	Val	Ala	Leu	His	Leu	Ala	Val	Gln	Ser	Leu	Arg	Arg	Gly	
		210					215					220					
	Glu	Cys	Asp	Leu	Ala	Leu	Ala	Gly	Gly	Val	Ala	Val	Met	Pro	Asp	Pro	
	225					230					235					240	
15	Thr	Val	Phe	Val	Glu	Phe	Ser	Arg	Gln	Arg	Gly	Leu	Ala	Val	Asp	Gly	
					245					250					255		
	Arg	Cys	Lys	Ala	Phe	Ala	Glu	Gly	Ala	Asp	Gly	Thr	Ala	Trp	Ala	Glu	
				260					265					270			
20	Gly	Val	Gly	Val	Leu	Leu	Val	Glu	Arg	Leu	Ser	Asp	Ala	Arg	Arg	Asn	
			275					280					285				
	Gly	His	Arg	Val	Leu	Ala	Val	Val	Arg	Gly	Ser	Ala	Val	Asn	Gln	Asp	
		290					295					300					
25	Gly	Ala	Ser	Asn	Gly	Leu	Thr	Ala	Pro	Ser	Gly	Pro	Ala	Gln	Gln	Arg	
	305					310					315					320	
	Val	Ile	Arg	Glu	Ala	Leu	Ala	Asp	Ala	Gly	Leu	Thr	Pro	Ala	Asp	Val	
					325					330					335		
30	Asp	Val	Val	Glu	Ala	His	Gly	Thr	Gly	Thr	Ala	Leu	Gly	Asp	Pro	Ile	
				340					345					350			
	Glu	Ala	Gly	Ala	Leu	Leu	Ala	Thr	Tyr	Gly	Arg	Glu	Arg	Val	Gly	Asp	
			355					360					365				
35	Pro	Leu	Trp	Leu	Gly	Ser	Leu	Lys	Ser	Asn	Ile	Gly	His	Ala	Gln	Ala	
		370					375					380					
	Ala	Ala	Gly	Val	Gly	Gly	Val	Ile	Lys	Val	Val	Gln	Ala	Met	Arg	His	
40	385					390					395					400	
	Gly	Ser	Leu	Pro	Arg	Thr	Leu	His	Val	Asp	Ala	Pro	Ser	Ser	Lys	Val	
					405					410					415		
45	Glu	Trp	Ala	Ser	Gly	Ala	Val	Glu	Leu	Leu	Thr	Glu	Gly	Arg	Ser	Trp	
			420					425						430			
	Pro	Arg	Arg	Val	Glu	Arg	Val	Arg	Arg	Ala	Ala	Val	Ser	Ala	Phe	Gly	
			435					440					445				
50	Val	Ser	Gly	Thr	Asn	Ala	His	Val	Val	Leu	Glu	Glu	Ala	Pro	Val	Glu	
		450					455					460					
	Ala	Gly	Ser	Glu	His	Gly	Asp	Gly	Pro	Gly	Pro	Asp	Arg	Pro	Asp	Ala	
	465					470					475					480	
55	Val	Thr	Gly	Pro	Leu	Pro	Trp	Val	Leu	Ser	Ala	Arg	Ser	Arg	Glu	Ala	

EP 0 791 655 A2

	485	490	495
5	Leu Arg Gly Gln Ala Gly Arg Leu Ala Ala Leu Ala Arg Gln Gly Arg 500 505 510		
	Thr Glu Gly Thr Gly Gly Gly Ser Gly Leu Val Val Pro Ala Ala Asp 515 520 525		
10	Ile Gly Tyr Ser Leu Ala Thr Thr Arg Glu Thr Leu Glu His Arg Ala 530 535 540		
	Val Ala Leu Val Gln Glu Asn Arg Thr Ala Gly Glu Asp Leu Ala Ala 545 550 555 560		
15	Leu Ala Ala Gly Arg Thr Pro Glu Ser Val Val Thr Gly Val Ala Arg 565 570 575		
	Arg Gly Arg Gly Ile Ala Phe Leu Cys Ser Gly Gln Gly Ala Gln Arg 580 585 590		
20	Leu Gly Ala Gly Arg Glu Leu Arg Gly Arg Phe Pro Val Phe Ala Asp 595 600 605		
	Ala Leu Asp Glu Ile Ala Ala Glu Phe Asp Ala His Leu Glu Arg Pro 610 615 620		
25	Leu Leu Ser Val Met Phe Ala Glu Pro Ala Thr Pro Asp Ala Ala Leu 625 630 635 640		
	Leu Asp Arg Thr Asp Tyr Thr Gln Pro Ala Leu Phe Ala Val Glu Thr 645 650 655		
30	Ala Leu Phe Arg Leu Leu Glu Ser Trp Gly Leu Val Pro Asp Val Leu 660 665 670		
	Val Gly His Ser Ile Gly Gly Leu Val Ala Ala His Val Ala Gly Val 675 680 685		
35	Phe Ser Ala Ala Asp Ala Ala Arg Leu Val Ser Ala Arg Gly Arg Leu 690 695 700		
	Met Arg Ala Leu Pro Glu Gly Gly Ala Met Ala Ala Val Gln Ala Thr 705 710 715 720		
40	Glu Arg Glu Ala Ala Ala Leu Glu Pro Val Ala Ala Gly Gly Ala Val 725 730 735		
	Val Ala Ala Val Asn Gly Pro Gln Ala Leu Val Leu Ser Gly Asp Glu 740 745 750		
45	Ala Ala Val Leu Ala Ala Ala Gly Glu Leu Ala Ala Arg Gly Arg Arg 755 760 765		
	Thr Lys Arg Leu Arg Val Ser His Ala Phe His Ser Pro Arg Met Asp 770 775 780		
50	Ala Met Leu Ala Asp Phe Arg Ala Val Ala Asp Thr Val Asp Tyr His 785 790 795 800		
55	Ala Pro Arg Leu Pro Val Val Ser Glu Val Thr Gly Asp Leu Ala Asp 805 810 815		

EP 0 791 655 A2

Ala Ala Gln Leu Thr Asp Pro Gly Tyr Trp Thr Arg Gln Val Arg Gln
820 825 830

5 Pro Val Arg Phe Ala Asp Ala Val Arg Thr Ala Ser Ala Arg Asp Ala
835 840 845

Ala Thr Phe Ile Glu Leu Gly Pro Asp Ala Val Leu Cys Gly Met Ala
850 855 860

10 Glu Glu Ser Leu Ala Ala Glu Ala Asp Val Val Phe Ala Pro Ala Leu
865 870 875 880

Arg Arg Gly Arg Pro Glu Gly Asp Thr Val Leu Arg Ala Ala Ala Ser
885 890 895

15 Ala Tyr Val Arg Gly Ala Gly Leu Asp Trp Ala Ala Leu Tyr Gly Gly
900 905 910

Thr Gly Ala Arg Arg Thr Asp Leu Pro Thr Tyr Ala Phe Gln His Ser
915 920 925

20 Arg Tyr Trp Leu Ala Pro Ala Ser Ala Ala Val Ala Pro Ala Thr Ala
930 935 940

25 Ala Pro Ser Val Arg Ser Val Pro Glu Ala Glu Gln Asp Gly Ala Leu
945 950 955 960

Trp Ala Ala Val His Ala Gly Asp Val Ala Ser Ala Ala Ala Arg Leu
965 970 975

30 Gly Ala Asp Asp Ala Gly Ile Glu His Glu Leu Arg Ala Val Leu Pro
980 985 990

His Leu Ala Ala Trp His Asp Arg Asp Arg Ala Thr Ala Arg Thr Ala
995 1000 1005

35 Gly Leu His Tyr Arg Val Thr Trp Gln Ala Ile Glu Ala Asp Ala Val
1010 1015 1020

Arg Phe Ser Pro Ser Asp Arg Trp Leu Met Val Glu His Gly Gln His
1025 1030 1035 1040

40 Thr Glu Cys Ala Asp Ala Ala Glu Arg Ala Leu Arg Ala Ala Gly Ala
1045 1050 1055

Glu Val Thr Arg Leu Val Trp Pro Leu Glu Gln His Thr Gly Ser Pro
1060 1065 1070

45 Arg Thr Glu Thr Pro Asp Arg Gly Thr Leu Ala Ala Arg Leu Ala Glu
1075 1080 1085

Leu Ala Arg Ser Pro Glu Gly Leu Ala Gly Val Leu Leu Leu Pro Asp
1090 1095 1100

50 Ser Gly Gly Ala Ala Val Ala Gly His Pro Gly Leu Asp Gln Gly Thr
1105 1110 1115 1120

Ala Ala Val Leu Leu Thr Ile Gln Ala Leu Thr Asp Ala Ala Val Arg
1125 1130 1135

55

EP 0 791 655 A2

Ala Pro Leu Trp Val Val Thr Arg Gly Ala Val Ala Val Gly Ser Gly
1140 1145 1150

5 Glu Val Pro Cys Ala Val Gly Ala Arg Val Trp Gly Leu Gly Arg Val
1155 1160 1165

Ala Ala Leu Glu Val Pro Val Gln Trp Gly Gly Leu Val Asp Val Ala
1170 1175 1180

10 Val Gly Ala Gly Val Arg Glu Trp Arg Arg Val Val Gly Val Val Ala
1185 1190 1195 1200

Gly Gly Gly Glu Asp Gln Val Ala Val Arg Gly Gly Gly Val Phe Gly
1205 1210 1215

15 Arg Arg Leu Val Gly Val Gly Val Arg Gly Gly Ser Gly Val Trp Arg
1220 1225 1230

Ala Arg Gly Cys Val Val Val Thr Gly Gly Leu Gly Gly Val Gly Gly
1235 1240 1245

20 His Val Ala Arg Trp Leu Ala Arg Ser Gly Ala Glu His Val Val Leu
1250 1255 1260

Ala Gly Arg Arg Gly Gly Gly Val Val Gly Ala Val Glu Leu Glu Arg
1265 1270 1275 1280

25 Glu Leu Val Gly Leu Gly Ala Lys Val Thr Phe Val Ser Cys Asp Val
1285 1290 1295

Gly Asp Arg Ala Ser Val Val Gly Leu Leu Gly Val Val Glu Gly Leu
1300 1305 1310

30 Gly Val Pro Leu Arg Gly Val Phe His Ala Ala Gly Val Ala Gln Val
1315 1320 1325

Ser Gly Leu Gly Glu Val Ser Leu Ala Glu Ala Gly Gly Val Leu Gly
1330 1335 1340

35 Gly Lys Ala Val Gly Ala Glu Leu Leu Asp Glu Leu Thr Ala Gly Val
1345 1350 1355 1360

Glu Leu Asp Ala Phe Val Leu Phe Ser Ser Gly Ala Gly Val Trp Gly
1365 1370 1375

40 Ser Gly Gly Gln Ser Val Tyr Ala Ala Ala Asn Ala His Leu Asp Ala
1380 1385 1390

Leu Ala Glu Arg Arg Arg Ala Gln Gly Arg Pro Ala Thr Ser Val Ala
1395 1400 1405

45 Trp Gly Pro Trp Asp Gly Asp Gly Met Gly Glu Met Ala Pro Glu Gly
1410 1415 1420

50 Tyr Phe Ala Arg His Gly Val Ala Pro Leu His Pro Glu Thr Ala Leu
1425 1430 1435 1440

Thr Ala Leu His Gln Ala Ile Asp Gly Gly Glu Ala Thr Val Thr Val
1445 1450 1455

55 Ala Asp Ile Asp Trp Glu Arg Phe Ala Pro Gly Phe Thr Ala Phe Arg

EP 0 791 655 A2

	1460	1465	1470
5	Pro Ser Pro Leu Ile Ala Gly 1475	Ile Pro Ala Ala Arg 1480	Thr Ala Pro Ala 1485
	Ala Gly Arg Pro Ala Glu Asp Thr 1490	Pro Thr Ala 1495	Pro Gly Leu Leu Arg 1500
10	Ala Arg Pro Glu Asp Arg Pro Arg 1505	Leu Ala 1510	Leu Asp Leu Val Leu Arg 1515 1520
	His Val Ala Ala Val Leu Gly 1525	His Ser Glu Asp Ala Arg 1530	Val Asp Ala 1535
15	Arg Ala Pro Phe Arg Asp Leu Gly 1540	Phe Asp Ser Leu Ala Ala Val Arg 1545	
	Leu Arg Arg Arg Leu Ala Glu Asp Thr Gly Leu Asp Leu Pro Gly Thr 1555		1560 1565
20	Leu Val Phe Asp His Glu Asp Pro Thr Ala Leu Ala His His Leu Ala 1570		1575 1580
	Gly Leu Ala Asp Ala Gly Thr Pro Gly Pro Gln Glu Gly Thr Ala Arg 1585		1590 1595 1600
25	Ala Glu Ser Gly Leu Phe Ala Ser Phe Arg Ala Ala Val Glu Gln Arg 1605		1610 1615
	Arg Ser Ser Glu Val Val Glu Leu Met Ala Asp Leu Ala Ala Phe Arg 1620		1625 1630
30	Pro Ala Tyr Ser Arg Gln His Pro Gly Ser Gly Arg Pro Ala Pro Val 1635		1640 1645
	Pro Leu Ala Thr Gly Pro Ala Thr Arg Pro Thr Leu Tyr Cys Cys Ala 1650		1655 1660
35	Gly Thr Ala Val Gly Ser Gly Pro Ala Glu Tyr Val Pro Phe Ala Glu 1665		1670 1675 1680
	Gly Leu Arg Gly Val Arg Glu Thr Val Ala Leu Pro Leu Ser Gly Phe 1685		1690 1695
40	Gly Asp Pro Ala Glu Pro Met Pro Ala Ser Leu Asp Ala Leu Ile Glu 1700		1705 1710
	Val Gln Ala Asp Val Leu Leu Glu His Thr Ala Gly Lys Pro Phe Ala 1715		1720 1725
45	Leu Ala Gly His Ser Ala Gly Ala Asn Ile Ala His Ala Leu Ala Ala 1730		1735 1740
	Arg Leu Glu Glu Arg Gly Ser Gly Pro Ala Ala Val Val Leu Met Asp 1745		1750 1755 1760
50	Val Tyr Arg Pro Glu Asp Pro Gly Ala Met Gly Glu Trp Arg Asp Asp 1765		1770 1775
	Leu Leu Ser Trp Ala Leu Glu Arg Ser Thr Val Pro Leu Glu Asp His 1780		1785 1790

Arg Leu Thr Ala Met Ala Gly Tyr Gln Arg Leu Val Leu Gly Thr Arg
 1795 1800 1805

5 Leu Thr Ala Leu Glu Ala Pro Val Leu Leu Ala Arg Ala Ser Glu Pro
 1810 1815 1820

Leu Cys Ala Trp Pro Pro Ala Gly Gly Ala Arg Gly Asp Trp Arg Ser
 1825 1830 1835 1840

10 Gln Val Pro Phe Ala Arg Thr Val Ala Asp Val Pro Gly Asn His Phe
 1845 1850 1855

Thr Met Leu Thr Glu His Ala Arg His Thr Ala Ser Leu Val His Glu
 1860 1865 1870

15 Trp Leu Asp Ser Leu Pro His Gln Pro Gly Pro Ala Pro Leu Thr Gly
 1875 1880 1885

Gly Lys His
 1890

20

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13987 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 350..13987

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GACCGCTCGG GGAGACCTGA CATATTCGTC GCGAAGTGGT TGTCCGCGCC GCGAGGTACT 60

GAAATCTTCT CCGCTCGCCC AGGACTCCGC GTGCAGGTCA CCGGAGTGCG CGACCGGCCG 120

GGACGTCGGA GCGCCGACCC TCGGACCTG GTGCGATGCC GTGTGGTCCC GCATGATCCC 180

GCGCCGTCTC CGGTGACGAG AATCGGTGGA CAATCTCCGA ACTTGACACA ATTGATTGTC 240

45 GTTCACCGGC CGTTCCTGTC GCCC GGCACT TCGCCGCTG TACGCTCGGG AAGATCAAGA 300

AAAGGCAGAA AAGCCACGGC GTGGTACGGC GAACATATGA GGGATGCAG GTG TCT 355

Met Ser
 1

50 GGA GAA CTC GCG ATT TCC CGC AGT GAC GAC CGG TCC GAC GCC GTT GCC 403

Gly Glu Leu Ala Ile Ser Arg Ser Asp Asp Arg Ser Asp Ala Val Ala
 5 10 15

55 GTG GTC GGA ATG GCG TGC CGG TTT CCC GGC GCC CCG GGA ATT GCC GAA 451

Val Val Gly Met Ala Cys Arg Phe Pro Gly Ala Pro Gly Ile Ala Glu

EP 0 791 655 A2

	20		25		30																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																															
--	----	--	----	--	----	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--

EP 0 791 655 A2

	260	265	270	
5	GCG CAG GAA GCT GTG CTG CGC CAG GCC TAC CGG CGG GCG GGC GTC AGC Ala Gln Glu Ala Val Leu Arg Gln Ala Tyr Arg Arg Ala Gly Val Ser 275 280 285 290	1219		
10	ACC GGC GCC GTC CGC TAC GTC GAG CTG CAC GGG ACC GGC ACC CGG GCC Thr Gly Ala Val Arg Tyr Val Glu Leu His Gly Thr Gly Thr Arg Ala 295 300 305	1267		
15	GGC GAC CCC GTC GAG GCG GCC GCA CTG GGC GCC GTG CTC GGG GCG GGG Gly Asp Pro Val Glu Ala Ala Leu Gly Ala Val Leu Gly Ala Gly 310 315 320	1315		
20	GCG GAC AGC GGC CGC AGC ACG CCG CTC GCC GTC GGC TCG GTG AAG ACC Ala Asp Ser Gly Arg Ser Thr Pro Leu Ala Val Gly Ser Val Lys Thr 325 330 335	1363		
25	AAC GTC GGC CAT CTG GAG GGC GCG GCG GGC ATC GTC GGA CTG ATC AAG Asn Val Gly His Leu Glu Gly Ala Ala Gly Ile Val Gly Leu Ile Lys 340 345 350	1411		
30	GCC ACG CTG TGC GTA CGG AAG GGC GAA CTC GTC CCC AGC CTC AAC TTC Ala Thr Leu Cys Val Arg Lys Gly Glu Leu Val Pro Ser Leu Asn Phe 355 360 365 370	1459		
35	AGC ACG CCG AAC CCT GAC ATC CCC CTC GAC GAC CTG CGG CTG CGC GTC Ser Thr Pro Asn Pro Asp Ile Pro Leu Asp Asp Leu Arg Leu Arg Val 375 380 385	1507		
40	CAG ACC GAA CGG CAG GAG TGG AAC GAG GAG GAC GAC CGG CCG CGC GTG Gln Thr Glu Arg Gln Glu Trp Asn Glu Glu Asp Asp Arg Pro Arg Val 390 395 400	1555		
45	GCC GGC GTC TCC TCC TTC GGT ATG GGC GGA ACC AAT GTC CAC CTC GTG Ala Gly Val Ser Ser Phe Gly Met Gly Gly Thr Asn Val His Leu Val 405 410 415	1603		
50	ATC GCG GAG GCT CCG GCC GCG GCG GGG TCC TCC GGG GCG GGG GGT TCG Ile Ala Glu Ala Pro Ala Ala Ala Gly Ser Ser Gly Ala Gly Gly Ser 420 425 430	1651		
55	GGC GCT GGT TCC GGT GCC GGT ATC AGC GCT GTT TCT GGT GTG GTG CCG Gly Ala Gly Ser Gly Ala Gly Ile Ser Ala Val Ser Gly Val Val Pro 435 440 445 450	1699		
60	GTG GTG GTT TCG GGG CGT TCG CGG GTG GTG GTG CGG GAG GCT GCG GGC Val Val Val Ser Gly Arg Ser Arg Val Val Val Arg Glu Ala Ala Gly 455 460 465	1747		
65	CGG TTG GCG GAG GTG GTG GAG GCC GGT GGT GTG GGG CTG GCG GAT GTC Arg Leu Ala Glu Val Val Glu Ala Gly Gly Val Gly Leu Ala Asp Val 470 475 480	1795		
70	GCG GTG ACG ATG GCG GAC CGG TCG CGG TTT GGG TAT CCG GCG GTT GTG Ala Val Thr Met Ala Asp Arg Ser Arg Phe Gly Tyr Arg Ala Val Val 485 490 495	1843		
75	CTG GCT CGG GGT GAG GCT GAG CTT GCC GGG CGT TTG CCG GCG TTG GCG Leu Ala Arg Gly Glu Ala Glu Leu Ala Gly Arg Leu Arg Ala Leu Ala	1891		

EP 0 791 655 A2

	500	505	510	
5	GGG GGT GAT CCG GAC GCG GGT GTG GTC ACC GGT GCG GTT CTC GAC GGT Gly Gly Asp Pro Asp Ala Gly Val Val Thr Gly Ala Val Leu Asp Gly 515 520 525 530			1939
10	GGT GTG GTT GTC GGT GCT GCC CCC GGC GGT GCC GGT GCT GCC GGT GGT Gly Val Val Val Gly Ala Ala Pro Gly Gly Ala Gly Ala Ala Gly Gly 535 540 545			1987
15	GCC GGT GCT GCC GGT GGT GCC GGT GGT GCG GCG GTG GTG TTG GTT TTC Ala Gly Ala Ala Gly Gly Ala Gly Gly Gly Val Val Leu Val Phe 550 555 560			2035
20	CCT GGT CAG GGG ACG CAG TGG GTG GGG ATG GGT GCG GGG CTG CTG GGG Pro Gly Gln Gly Thr Gln Trp Val Gly Met Gly Ala Gly Leu Leu Gly 565 570 575			2083
25	TCT TCG GAG GTG TTT GCG GCG TCG ATG CCG GAG TGT GCG CCG GCG CTG Ser Ser Glu Val Phe Ala Ala Ser Met Arg Glu Cys Ala Arg Ala Leu 580 585 590			2131
30	AGT GTT CAT GTG GGG TGG GAT TTG CTG GAG GTG GTG TCG GCG GCG GCC Ser Val His Val Gly Trp Asp Leu Leu Glu Val Val Ser Gly Gly Ala 595 600 605 610			2179
35	GGG TTG GAG CCG GTG GAT GTG GTG CAG CCG GTG ACG TGG GCG GTG ATG Gly Leu Glu Arg Val Asp Val Val Gln Pro Val Thr Trp Ala Val Met 615 620 625			2227
40	GTG TCG CTG GCC CCG TAC TGG CAG GCG ATG GGT GTG GAC GTG GCT GCG Val Ser Leu Ala Arg Tyr Trp Gln Ala Met Gly Val Asp Val Ala Ala 630 635 640			2275
45	GTG GTG GGT CAT TCC CAG GGG GAG ATC GCC GCT GCC ACG GTG GCG GGG Val Val Gly His Ser Gln Gly Glu Ile Ala Ala Ala Thr Val Ala Gly 645 650 655			2323
50	GCG TTG TCG CTG GAG GAT GCG GCG GCT GTG GTC GCT CTG CCG GCG GGG Ala Leu Ser Leu Glu Asp Ala Ala Ala Val Val Ala Leu Arg Ala Gly 660 665 670			2371
55	TTG ATT GGC CCG TAT CTG GCG GGT CGT GGT GCG ATG GCG GCT GTT CCG Leu Ile Gly Arg Tyr Leu Ala Gly Arg Gly Ala Met Ala Ala Val Pro 675 680 685 690			2419
60	CTG CCT GCC GGC GAG GTC GAG GCC GGG CTG GCG AAG TGG CCG GGT GTG Leu Pro Ala Gly Glu Val Glu Ala Gly Leu Ala Lys Trp Pro Gly Val 695 700 705			2467
65	GAG GTC GCG GCG GTC AAC GGT CCG GCG TCT ACG GTG GTT TCC GCG GAT Glu Val Ala Ala Val Asn Gly Pro Ala Ser Thr Val Val Ser Gly Asp 710 715 720			2515
70	CGG CCG GCG GTG GCC GGT TAT GTG GCC GTC TGT CAG CCG GAG GGT GTG Arg Arg Ala Val Ala Gly Tyr Val Ala Val Cys Gln Ala Glu Gly Val 725 730 735			2563
75	CAG GCC CCG TTG ATA CCG GTG GAC TAC GCC TCT CAC TCC CCG CAT GTG Gln Ala Arg Leu Ile Pro Val Asp Tyr Ala Ser His Ser Arg His Val			2611

EP 0 791 655 A2

	740	745	750	
5	GAG GAC CTG AAG GGC GAG TTG GAG CGG GTG CTG TCC GGT ATC CGC CCC Glu Asp Leu Lys Gly Glu Leu Glu Arg Val Leu Ser Gly Ile Arg Pro 755 760 765 770	2659		
10	CGC AGT CCG CGG GTG CCG GTG TGT TCC ACC GTC GCC GGA GAG CAG CCG Arg Ser Pro Arg Val Pro Val Cys Ser Thr Val Ala Gly Glu Gln Pro 775 780 785	2707		
15	GGC GAG CCG GTT TTC GAT GCG GGG TAT TGG TTC CGT AAT CTG CGG AAC Gly Glu Pro Val Phe Asp Ala Gly Tyr Trp Phe Arg Asn Leu Arg Asn 790 795 800	2755		
20	CGG GTT GAG TTC TCC GCG GTG GTC GGT GGT TTG TTG GAG GAG GGC CAC Arg Val Glu Phe Ser Ala Val Gly Gly Leu Leu Glu Glu Gly His 805 810 815	2803		
25	CGT CGG TTC ATC GAG GTC AGT GCC CAC CCG GTA CTC GTC CAT GCG ATC Arg Arg Phe Ile Glu Val Ser Ala His Pro Val Leu Val His Ala Ile 820 825 830	2851		
30	GAG CAG ACG GCC GAG GCC GCG GAC CGG AGT GTC CAT GCC ACC GGG ACC Glu Gln Thr Ala Glu Ala Ala Asp Arg Ser Val His Ala Thr Gly Thr 835 840 845 850	2899		
35	CTG CGC CGC CAG GAC GAC ACC CCG CAC CGC CTG CTG ACC TCC ACC GCC Leu Arg Arg Gln Asp Asp Ser Pro His Arg Leu Leu Thr Ser Thr Ala 855 860 865	2947		
40	GAG GCC TGG GCC CAC GGC GCC ACC CTC ACC TGG GAC CCC GCC CTG CCC Glu Ala Trp Ala His Gly Ala Thr Leu Thr Trp Asp Pro Ala Leu Pro 870 875 880	2995		
45	CCA GGC CAC CTC ACC ACC CTC CCC ACC TAC CCC TTC AAC CAC CAC CAC Pro Gly His Leu Thr Thr Leu Pro Thr Tyr Pro Phe Asn His His His 885 890 895	3043		
50	TAC TGG CTC GAC ACC ATT GAC GGG GGC GGA GGG GAC GAC GCG ACC CAG Tyr Trp Leu Asp Thr Ile Asp Gly Gly Gly Gly Asp Asp Ala Thr Gln 900 905 910	3091		
55	GAG AAG GAG AGC GGC CCT CTG ACG CGG GAA CTG CGT GGG CTG CCG TCC Glu Lys Glu Ser Gly Pro Leu Thr Arg Glu Leu Arg Gly Leu Pro Ser 915 920 925 930	3139		
60	TCT CAG AAG CAA CTG GGT TTC CTG CTC GAT CTG GTG TGC CGG CAC ACG Ser Gln Lys Gln Leu Gly Phe Leu Leu Asp Leu Val Cys Arg His Thr 935 940 945	3187		
65	GCC GTC GTA CTC GGC CTG GAC ACG GCC GCC GAG GTG GAC CCG GAC CTG Ala Val Val Leu Gly Leu Asp Thr Ala Ala Glu Val Asp Pro Asp Leu 950 955 960	3235		
70	TCC TTC AAG AAG CAG GGC ATC CAG TCC ATG ACC GGC GTC GAG CTG CGC Ser Phe Lys Lys Gln Gly Ile Gln Ser Met Thr Gly Val Glu Leu Arg 965 970 975	3283		
75	AAC AGG CTG CTG ACC GAG ACC GGC CTG GCA TTG CCC ACC ACC CTC GTC Asn Arg Leu Leu Thr Glu Thr Gly Leu Ala Leu Pro Thr Thr Leu Val	3331		

EP 0 791 655 A2

	980	985	990	
5	TAC GAC CGG CCC ACC CCT CGC GCC CTG GCG CAG TTC CTC CAC ACC GAG Tyr Asp Arg Pro Thr Pro Arg Ala Leu Ala Gln Phe Leu His Thr Glu 995 1000 1005 1010	3379		
10	TTG CTC GAC GGC TCC CCC TCG GGC TCC GTC CTC GCA CCG GCG CAG AAG Leu Leu Asp Gly Ser Pro Ser Gly Ser Val Leu Ala Pro Ala Gln Lys 1015 1020 1025	3427		
15	AGC TTC GAG GCC GGC GGG CCC GGA GTG CTC TCG TCG GCC GCG GTA GGG Ser Phe Glu Ala Gly Gly Pro Gly Val Leu Ser Ser Ala Ala Val Gly 1030 1035 1040	3475		
20	GTG TCG GAC GCC CGG GGC GGC AGC CGG GAC GAC GAC GAC CCG ATC GCC Val Ser Asp Ala Arg Gly Gly Ser Arg Asp Asp Asp Pro Ile Ala 1045 1050 1055	3523		
25	ATC GTG GGT GTC GGC TGC CGG CTC CCC GGC GGC GTC GAC TCG CGC GCC Ile Val Gly Val Gly Cys Arg Leu Pro Gly Gly Val Asp Ser Arg Ala 1060 1065 1070	3571		
30	GCT CTC TGG GAG CTG CTG GAG TCC GGC GCC GAC GCC ATC TCG TCC TTC Ala Leu Trp Glu Leu Leu Glu Ser Gly Ala Asp Ala Ile Ser Ser Phe 1075 1080 1085 1090	3619		
35	CCC ACC GAC CGC GGC TGG GAC CTC GAC GGG CTG TAC GAC CCC GAG CCC Pro Thr Asp Arg Gly Trp Asp Leu Asp Gly Leu Tyr Asp Pro Glu Pro 1095 1100 1105	3667		
40	GGG ACG CCC GGC AAG ACC TAT GTG CGG GAG GGC GGG TTC CTG CAC TCG Gly Thr Pro Gly Lys Thr Tyr Val Arg Glu Gly Gly Phe Leu His Ser 1110 1115 1120	3715		
45	GCG GCC GAG TTC GAC GCG GAG TTC TTC GGG ATA TCG CCG CGC GAG GCC Ala Ala Glu Phe Asp Ala Glu Phe Phe Gly Ile Ser Pro Arg Glu Ala 1125 1130 1135	3763		
50	ACG GCC ATG GAC CCG CAG CAG CGC TTG CTG CTG GAA GCG TCG TGG GAG Thr Ala Met Asp Pro Gln Gln Arg Leu Leu Leu Glu Ala Ser Trp Glu 1140 1145 1150	3811		
55	GCC CTC GAG GAC GCC GGA GTG CTC CCC GAG TCA CTG CGC GGC GGC GAC Ala Leu Glu Asp Ala Gly Val Leu Pro Glu Ser Leu Arg Gly Gly Asp 1155 1160 1165 1170	3859		
60	GCC GGA GTG TTC GTC GGC GCC ACC GCA CCG GAG TAC GGG CCG AGG CTT Ala Gly Val Phe Val Gly Ala Thr Ala Pro Glu Tyr Gly Pro Arg Leu 1175 1180 1185	3907		
65	CAC GAG GGA GCG GAC GGA TAC GAG GGG TAC CTG CTC ACC GGC ACC ACC His Glu Gly Ala Asp Gly Tyr Glu Gly Tyr Leu Leu Thr Gly Thr Thr 1190 1195 1200	3955		
70	GCG AGC GTG GCC TCC GGC CGG ATC GCC TAC ACC CTC GGC ACC GGC GGA Ala Ser Val Ala Ser Gly Arg Ile Ala Tyr Thr Leu Gly Thr Gly Gly 1205 1210 1215	4003		
75	CCG GCG CTC ACC GTC GAC ACC GCG TGC TCC TCG TCC CTG GTG GCG CTG Pro Ala Leu Thr Val Asp Thr Ala Cys Ser Ser Ser Leu Val Ala Leu	4051		

EP 0 791 655 A2

	1220	1225	1230	
5	CAC CTG GCC GTG CAG GCG CTG CGC CGG GGC GAG TGC GGG CTG GCT CTG His Leu Ala Val Gln Ala Leu Arg Arg Gly Glu Cys Gly Leu Ala Leu 1235 1240 1245 1250			4099
10	GCG GGC GGC GCC ACG GTG ATG TCG GGG CCC GGC ATG TTC GTG GAG TTC Ala Gly Gly Ala Thr Val Met Ser Gly Pro Gly Met Phe Val Glu Phe 1255 1260 1265			4147
15	TCG CGG CAG CGC GGG CTC GCC CCC GAC GGC CGC TGC ATG CCG TTC TCC Ser Arg Gln Arg Gly Leu Ala Pro Asp Gly Arg Cys Met Pro Phe Ser 1270 1275 1280			4195
20	GCC GAT GCC GAC GGT ACG GCC TGG TCC GAG GGT GTC GCC GTA CTG GCA Ala Asp Ala Asp Gly Thr Ala Trp Ser Glu Gly Val Ala Val Leu Ala 1285 1290 1295			4243
25	CTG GAG CGG CTC TCC GAC GCC CGG CGT GCG GGA CAC CGG CTG CTG GGC Leu Glu Arg Leu Ser Asp Ala Arg Arg Ala Gly His Arg Val Leu Gly 1300 1305 1310			4291
30	GTG GTG CGG GGC AGT GCG GTC AAC CAG GAC GGT GCC AGC AAC GGC CTG Val Val Arg Gly Ser Ala Val Asn Gln Asp Gly Ala Ser Asn Gly Leu 1315 1320 1325 1330			4339
35	ACC GCT CCC AAC CGC TCC GCG CAG GAG GGC GTC ATC CGA GCT GCC CTG Thr Ala Pro Asn Arg Ser Ala Gln Glu Gly Val Ile Arg Ala Ala Leu 1335 1340 1345			4387
40	GCC GAC GCC GGC CTC GCG CCG GGT GAC GTG GAC GCG GTG GAG GCG CAC Ala Asp Ala Gly Leu Ala Pro Gly Asp Val Asp Ala Val Glu Ala His 1350 1355 1360			4435
45	GGT ACG GGG ACG GCG CTG GGC GAT CCG ATC GAG GCG AGC GCG CTG CTG Gly Thr Gly Thr Ala Leu Gly Asp Pro Ile Glu Ala Ser Ala Leu Leu 1365 1370 1375			4483
50	GCC ACG TAC GGG CGT GAG CCG GTG GGC GAC CCC TTG TGG CTC GGG TCG Ala Thr Tyr Gly Arg Glu Arg Val Gly Asp Pro Leu Trp Leu Gly Ser 1380 1385 1390			4531
55	CTG AAG TCC AAC GTC GGT CAC ACC CAG GCC GCC GCG GGG GCC GCG GGT Leu Lys Ser Asn Val Gly His Thr Gln Ala Ala Ala Gly Ala Ala Gly 1395 1400 1405 1410			4579
60	GTG GTC AAG ATG CTG CTT GCC CTG GAG CAC GGC ACG CTG CCG CGG ACA Val Val Lys Met Leu Leu Ala Leu Glu His Gly Thr Leu Pro Arg Thr 1415 1420 1425			4627
65	CTT CAC GCG GAC CGG CCC AGC ACG CAC GTC GAC TGG TCG TCG GGC ACC Leu His Ala Asp Arg Pro Ser Thr His Val Asp Trp Ser Ser Gly Thr 1430 1435 1440			4675
70	GTC GCC CTG CTG GCA GAG GCG CCG CCG TGG CCC CGG CGG TCG GAC CGC Val Ala Leu Leu Ala Glu Ala Arg Arg Trp Pro Arg Arg Ser Asp Arg 1445 1450 1455			4723
75	CCG CGC CGG GCG GCT GTG TCG TCG TTC GGG ATC AGT GGG ACG AAC GCG Pro Arg Arg Ala Ala Val Ser Ser Phe Gly Ile Ser Gly Thr Asn Ala			4771

EP 0 791 655 A2

	1460	1465	1470	
5	CAT CTG ATC ATC GAG GAG GCG CCG GAG TGG GTC GAG GAC ATC GAC GGC His Leu Ile Ile Glu Glu Ala Pro Glu Trp Val Glu Asp Ile Asp Gly 1475 1480 1485 1490	4819		
10	GTC GCT GCT CCT GAC CGC GGT ACC GCG GAC GCG GCT GCT CCG TCG CCG Val Ala Ala Pro Asp Arg Gly Thr Ala Asp Ala Ala Ala Pro Ser Pro 1495 1500 1505	4867		
15	CTG TTG TTG TCC GCG CGG TCG GAG GGG GCG TTG CCG GCG CAG GCG GTG Leu Leu Leu Ser Ala Arg Ser Glu Gly Ala Leu Arg Ala Gln Ala Val 1510 1515 1520	4915		
20	CGG TTG GGT GAG TAC GTG GAG CGG GTG GGT GCG GAT CCG CCG GAT GTG Arg Leu Gly Glu Tyr Val Glu Arg Val Gly Ala Asp Pro Arg Asp Val 1525 1530 1535	4963		
25	GCT TAT TCG CTG GCT TCG ACG CGG ACT CTT TTC GAG CAC CGT GCG GTG Ala Tyr Ser Leu Ala Ser Thr Arg Thr Leu Phe Glu His Arg Ala Val 1540 1545 1550	5011		
30	GTG CCG TGT GGT GGG CGT GGG GAG CTC GTC GCT GCT CTT GGT GGG TTT Val Pro Cys Gly Gly Arg Gly Glu Leu Val Ala Ala Leu Gly Gly Phe 1555 1560 1565 1570	5059		
35	GCT GCC GGG AGG GTG TCT GGG GGT GTG CCG TCC GGG CCG GCT GTG CCG Ala Ala Gly Arg Val Ser Gly Gly Val Arg Ser Gly Arg Ala Val Pro 1575 1580 1585	5107		
40	GGT GGG GTG GGG GTG TTG TTC ACG GGT CAG GGT GCG CAG TGG GTT GGT Gly Gly Val Gly Val Leu Phe Thr Gly Gln Gly Ala Gln Trp Val Gly 1590 1595 1600	5155		
45	ATG GGG CGT GGG TTG TAT GCG GGG GGT GGG GTG TTT GCG GAG GTG CTG Met Gly Arg Gly Leu Tyr Ala Gly Gly Gly Val Phe Ala Glu Val Leu 1605 1610 1615	5203		
50	GAT GAG GTG TTG TCG ATG GTG GGG GAG GTG GAT GGT CCG TCG TTG CCG Asp Glu Val Leu Ser Met Val Gly Glu Val Asp Gly Arg Ser Leu Arg 1620 1625 1630	5251		
55	GAT GTG ATG TTC GGC GAC GTC GAC GTG GAC GCG GGT GCC GGG GCT GAT Asp Val Met Phe Gly Asp Val Asp Val Asp Ala Gly Ala Gly Ala Asp 1635 1640 1645 1650	5299		
60	GCG GGT GCC GGT GCG GGT GCT GGG GTC GGT TCT GGT TCC GGT TCT GTG Ala Gly Ala Gly Ala Gly Ala Gly Val Gly Ser Gly Ser Gly Ser Val 1655 1660 1665	5347		
65	GGT GGG TTG TTG GGT CCG ACG GAG TTT GCT CAG CCT GCG CTG TTT GCG Gly Gly Leu Leu Gly Arg Thr Glu Phe Ala Gln Pro Ala Leu Phe Ala 1670 1675 1680	5395		
70	TTG GAG GTG GCG TTG TTC CCG GCG TTG GAG GCT CCG GGT GTG GAG GTG Leu Glu Val Ala Leu Phe Arg Ala Leu Glu Ala Arg Gly Val Glu Val 1685 1690 1695	5443		
75	TCG GTG GTG TTG GGT CAT TCG GTG GGG GAG GTG GCT GCT GCG TAT GTG Ser Val Val Leu Gly His Ser Val Gly Glu Val Ala Ala Ala Tyr Val 1700 1705 1710	5491		

EP 0 791 655 A2

	1700	1705	1710	
5	GCG GGG GTG TTG TCG TTG GGT GAT GCG GTG CCG TTG GTG GTG GCG CCG Ala Gly Val Leu Ser Leu Gly Asp Ala Val Arg Leu Val Val Ala Arg 1715 1720 1725 1730			5539
10	GGT GGG TTG ATG GGT GGG TTG CCG GTG GGT GGG GGG ATG TGG TCG GTG Gly Gly Leu Met Gly Gly Leu Pro Val Gly Gly Gly Met Trp Ser Val 1735 1740 1745			5587
15	GGG GCG TCG GAG TCG GTG GTG CCG GGG GTT GTT GAG GGG TTG GGG GAG Gly Ala Ser Glu Ser Val Val Arg Gly Val Val Glu Gly Leu Gly Glu 1750 1755 1760			5635
20	TGG GTG TCG GTT CCG GCG GTG AAT GGG CCG CCG TCG GTG GTG TTG TCG Trp Val Ser Val Ala Ala Val Asn Gly Pro Arg Ser Val Val Leu Ser 1765 1770 1775			5683
25	GGT GAT GTG GGT GTG CTG GAG TCG GTG GTT GCC TCG CTG ATG GGG GAT Gly Asp Val Gly Val Leu Glu Ser Val Val Ala Ser Leu Met Gly Asp 1780 1785 1790			5731
30	GGG GTG GAG TGC CCG CCG TTG GAT GTG TCG CAT GGG TTT CAT TCG GTG Gly Val Glu Cys Arg Arg Leu Asp Val Ser His Gly Phe His Ser Val 1795 1800 1805 1810			5779
35	TTG ATG GAG CCG GTG TTG CCG GAG TTC CCG GGG GTT GTG GAG TCG TTG Leu Met Glu Pro Val Leu Gly Glu Phe Arg Gly Val Val Glu Ser Leu 1815 1820 1825			5827
40	GAG TTC GGT CCG GTG CCG CCG GGT GTG GTG GTG GTG TCG GGT GTG TCG Glu Phe Gly Arg Val Arg Pro Gly Val Val Val Val Ser Gly Val Ser 1830 1835 1840			5875
45	GGT GGG GTG GTG GGT TCG GGG GAG TTG GGG GAT CCG GGG TAT TGG GTG Gly Gly Val Val Gly Ser Gly Glu Leu Gly Asp Pro Gly Tyr Trp Val 1845 1850 1855			5923
50	CGT CAT GCG CCG GAG GCG GTG CGT TTC GCG GAT GGG GTG GGG GTG GTG Arg His Ala Arg Glu Ala Val Arg Phe Ala Asp Gly Val Gly Val Val 1860 1865 1870			5971
55	CGT GGT CTG GGT GTG GGG ACG TTG GTG GAG GTG GGT CCG CAT GGG GTG Arg Gly Leu Gly Val Gly Thr Leu Val Glu Val Gly Pro His Gly Val 1875 1880 1885 1890			6019
60	CTG ACG GGG ATG GCG GGT GAG TGC CTG GGG GCC GGT GAT GAT GTG GTG Leu Thr Gly Met Ala Gly Glu Cys Leu Gly Ala Gly Asp Asp Val Val 1895 1900 1905			6067
65	GTG GTG CCG GCG ATG CCG CCG GGC CGT GCG GAG CCG GAG GTG TTC GAG Val Val Pro Ala Met Arg Arg Gly Arg Ala Glu Arg Glu Val Phe Glu 1910 1915 1920			6115
70	GCG GCG CTG GCG ACG GTG TTC ACC CCG GAC GCC GCC CTG GAC GCC ACG Ala Ala Leu Ala Thr Val Phe Thr Arg Asp Ala Gly Leu Asp Ala Thr 1925 1930 1935			6163
75	GCA CTC CAC ACC GGG AGC ACC GGC CCG CGC ATC GAC CTC CCC ACC TAC Ala Leu His Thr Gly Ser Thr Gly Arg Arg Ile Asp Leu Pro Thr Tyr			6211

EP 0 791 655 A2

	1940	1945	1950	
5	CCC TTC CAA CGC GAC CGC TAC TGG CTG GAC CCC GTT CGC ACC GCC GTG Pro Phe Gln Arg Asp Arg Tyr Trp Leu Asp Pro Val Arg Thr Ala Val 1955 1960 1965 1970	6259		
10	ACC GGC GTC GAG CCC GCC GGC TCG CCG GCG GAC GCT CGG GCC ACT GAG Thr Gly Val Glu Pro Ala Gly Ser Pro Ala Asp Ala Arg Ala Thr Glu 1975 1980 1985	6307		
15	CGG GGA CGG TCG ACG ACG GCC GGG ATC CGC TAC CGC GTC GCT TGG CAG Arg Gly Arg Ser Thr Thr Ala Gly Ile Arg Tyr Arg Val Ala Trp Gln 1990 1995 2000	6355		
20	CCG GCC GTC GTC GAC CGC GGC AAC CCC GGG CCT GCC GGT CAT GTG CTG Pro Ala Val Val Asp Arg Gly Asn Pro Gly Pro Ala Gly His Val Leu 2005 2010 2015	6403		
25	CTT CTG GCC CCG GAC GAG GAC ACG GCC GAC TCC GGA CTC GCC CCC GCG Leu Leu Ala Pro Asp Glu Asp Thr Ala Asp Ser Gly Leu Ala Pro Ala 2020 2025 2030	6451		
30	ATC GCA CGT GAA CTC GCC GTG CGC GGG GCC GAG GTC CAC ACC GTC GCC Ile Ala Arg Glu Leu Ala Val Arg Gly Ala Glu Val His Thr Val Ala 2035 2040 2045 2050	6499		
35	GTG CCG GTC GGT ACA GGC CCG GAG GCA GCC GGG GAC CTG TTG CCG GCC Val Pro Val Gly Thr Gly Arg Glu Ala Ala Gly Asp Leu Leu Arg Ala 2055 2060 2065	6547		
40	GCC GGT GAC GGT GCC GCC CGC AGC ACC CGA GTT CTG TGG CTC GCC CCG Ala Gly Asp Gly Ala Ala Arg Ser Thr Arg Val Leu Trp Leu Ala Pro 2070 2075 2080	6595		
45	GCC GAG CCG GAC GCG GCC GAC GCC GTC GCC CTC GTC CAG GCG CTG GCG Ala Glu Pro Asp Ala Ala Asp Ala Val Ala Leu Val Gln Ala Leu Gly 2085 2090 2095	6643		
50	GAG GCG GTA CCC GAA GCC CCG CTC TGG ATC ACC ACC CGT GAG GCG GCG Glu Ala Val Pro Glu Ala Pro Leu Trp Ile Thr Thr Arg Glu Ala Ala 2100 2105 2110	6691		
55	GCC GTG CCG CCG GAC GAG ACC CCT TCC GTC GGG GGC GCT CAG CTG TGG Ala Val Arg Pro Asp Glu Thr Pro Ser Val Gly Gly Ala Gln Leu Trp 2115 2120 2125 2130	6739		
60	GGA CTC GGA CAG GTC GCC GCG CTC GAA CTG GGG CCG CGC TGG GGC GGC Gly Leu Gly Gln Val Ala Ala Leu Glu Leu Gly Arg Arg Trp Gly Gly 2135 2140 2145	6787		
65	TTG GCG GAC CTG CCC GGG AGT GCG TCG CCC GCG GTG CTC CGT ACG TTC Leu Ala Asp Leu Pro Gly Ser Ala Ser Pro Ala Val Leu Arg Thr Phe 2150 2155 2160	6835		
70	GTC GGG GCG CTG CTC GCC GGG GGA GAG AAC CAG TTC GCG GTA CCG CCC Val Gly Ala Leu Leu Ala Gly Gly Glu Asn Gln Phe Ala Val Arg Pro 2165 2170 2175	6883		
75	TCC GGC GTC CAT GTC CGC CGT GTG GTT CCC GCG CCC GTC CCC GTC CCG Ser Gly Val His Val Arg Arg Val Val Pro Ala Pro Val Pro Val Pro	6931		

EP 0 791 655 A2

	2180	2185	2190	
5	GCC TCC GCT CGC ACC GTC ACC ACG GCC CCC GCC ACC GCC GTC GGC GAG Ala Ser Ala Arg Thr Val Thr Thr Ala Pro Ala Thr Ala Val Gly Glu 2195 2200 2205 2210	6979		
	GAC GCA CGG AAC GAC ACC TCG GAC GTG GTC GTG CCG GAC GAC CGG TGG Asp Ala Arg Asn Asp Thr Ser Asp Val Val Val Pro Asp Asp Arg Trp 2215 2220 2225	7027		
10	TCC TCC GGC ACC GTA CTG ATC ACC GGG GGC ACC GGT GCC CTG GGT GCG Ser Ser Gly Thr Val Leu Ile Thr Gly Gly Thr Gly Ala Leu Gly Ala 2230 2235 2240	7075		
15	CAG GTC GCC CGC AGG CTC GCC CGG TCG GGC GCC GCG CGT CTG CTC CTG Gln Val Ala Arg Arg Leu Ala Arg Ser Gly Ala Ala Arg Leu Leu Leu 2245 2250 2255	7123		
20	GTG GGC CGG CGC GGC GCG GCC GGC CCC GGA GTG GGC GAA CTC GTC GAG Val Gly Arg Arg Gly Ala Ala Gly Pro Gly Val Gly Glu Leu Val Glu 2260 2265 2270	7171		
	GAG CTG ACG GCG CTC GGT TCC GAA GTG GCC GTC GAG GCC TGC GAC GTC Glu Leu Thr Ala Leu Gly Ser Glu Val Ala Val Glu Ala Cys Asp Val 2275 2280 2285 2290	7219		
25	GCC GAC CGG GAC GCA CTG GCC GCG CTC CTC GCG GGC CTC CCC GAG GAG Ala Asp Arg Asp Ala Leu Ala Ala Leu Leu Ala Gly Leu Pro Glu Glu 2295 2300 2305	7267		
30	CGG CCC CTC GTC GCC GTA CTG CAC GCG GCA GGT GTG CTC GAC GAC GGT Arg Pro Leu Val Ala Val Leu His Ala Ala Gly Val Leu Asp Asp Gly 2310 2315 2320	7315		
35	GTG CTC GAC TCG CTC ACC TCC GAC CGG GTG GAC GCC GTA CTG CGG GAC Val Leu Asp Ser Leu Thr Ser Asp Arg Val Asp Ala Val Leu Arg Asp 2325 2330 2335	7363		
	AAG GTC ACC GCC GCC CGT CAC CTG GAC GAG CTG ACC GCG GAC CTT CCG Lys Val Thr Ala Ala Arg His Leu Asp Glu Leu Thr Ala Asp Leu Pro 2340 2345 2350	7411		
40	CTC GAC GCC TTC GTG CTC TTC TCC TCC ATC GTC GGC GTG TGG GGC AAC Leu Asp Ala Phe Val Leu Phe Ser Ser Ile Val Gly Val Trp Gly Asn 2355 2360 2365 2370	7459		
45	GGA GGG CAG GCC GTC TAC GCG GCC GCC AAC GCC GCG CTC GAC GCC CTG Gly Gly Gln Ala Val Tyr Ala Ala Ala Asn Ala Ala Leu Asp Ala Leu 2375 2380 2385	7507		
	GCG CAG CGG CGC CGG GCC AGG GGA GCC CGT GCC GCC TCG ATC GCC TGG Ala Gln Arg Arg Arg Ala Arg Gly Ala Arg Ala Ala Ser Ile Ala Trp 2390 2395 2400	7555		
50	GGG CCG TGG GCC GGT GCC GGA ATG GCC TCC GGA ACG GCG GCG AAG TCC Gly Pro Trp Ala Gly Ala Gly Met Ala Ser Gly Thr Ala Ala Lys Ser 2405 2410 2415	7603		
55	TTC GAA CGG GAC GGC GTC ACG GCC CTG GAC CCC GAG CGC GCG CTC GAC Phe Glu Arg Asp Gly Val Thr Ala Leu Asp Pro Glu Arg Ala Leu Asp	7651		

EP 0 791 655 A2

	2420	2425	2430	
5	GTC CTC GAC GAC GTG GTG GGC GCC GGC GGG ACC TCT GCC GCA GGG ACG Val Leu Asp Asp Val Val Gly Ala Gly Gly Thr Ser Ala Ala Gly Thr 2435 2440 2445 2450			7699
	CAC GCG GCC GGC GAG AGC TCC CTG CTC GTC GCC GAC GTG GAC TGG GAG His Ala Ala Gly Glu Ser Ser Leu Leu Val Ala Asp Val Asp Trp Glu 2455 2460 2465			7747
10	ACC TTC GTC GGG CGT TCG GTC ACC CGC CGT ACC TGG TCG CTC TTC GAC Thr Phe Val Gly Arg Ser Val Thr Arg Arg Thr Trp Ser Leu Phe Asp 2470 2475 2480			7795
15	GGC GTC TCC GCC GCC CGT TCG GCG CGT GCC GGC CAT GCC GCG GAC GAC Gly Val Ser Ala Ala Arg Ser Ala Arg Ala Gly His Ala Ala Asp Asp 2485 2490 2495			7843
20	CGT GCC GCT CTC ACC CCA GGG ACG CGG CCG GGC GAC GGC GCA CCG GGC Arg Ala Ala Leu Thr Pro Gly Thr Arg Pro Gly Asp Gly Ala Pro Gly 2500 2505 2510			7891
	GGG AGC GGA CAG GAC GGG GGC GAG GGC CGG CCG TGG CTC TCC GTC GGC Gly Ser Gly Gln Asp Gly Gly Glu Gly Arg Pro Trp Leu Ser Val Gly 2515 2520 2525 2530			7939
25	CCC TCG CCG GCG GAA CGC CGT CGT GCT CTG CTC ACG CTT GTG CGC TCG Pro Ser Pro Ala Glu Arg Arg Arg Ala Leu Leu Thr Leu Val Arg Ser 2535 2540 2545			7987
30	GAG GCC GCC GGG ATC CTG CGC CAC GCC TCG GCC GAC GCG GTC GAC CCG Glu Ala Ala Gly Ile Leu Arg His Ala Ser Ala Asp Ala Val Asp Pro 2550 2555 2560			8035
35	GAG CTG GCC TTC CCG TCC GCC GGG TTC GAC TCC CTC ACC GTT CTC GAA Glu Leu Ala Phe Arg Ser Ala Gly Phe Asp Ser Leu Thr Val Leu Glu 2565 2570 2575			8083
	CTG CGT AAC CCG CTG ACC GCT GCC ACC GGC CTG AAC CTG CCG AAC ACG Leu Arg Asn Arg Leu Thr Ala Ala Thr Gly Leu Asn Leu Pro Asn Thr 2580 2585 2590			8131
40	CTG CTC TTC GAC CAC CCG ACC CCC CTC TCG CTC GCC TCC CAC CTG CAC Leu Leu Phe Asp His Pro Thr Pro Leu Ser Leu Ala Ser His Leu His 2595 2600 2605 2610			8179
45	GAC GAA CTG TTC GGT CCC GAC AGC GAG GCG GAG CCG GCA GCG GCC GCC Asp Glu Leu Phe Gly Pro Asp Ser Glu Ala Glu Pro Ala Ala Ala Ala 2615 2620 2625			8227
	CCC ACG CCG GTC ATG GCC GAC GAG CGT GAG CCG ATC GCG ATC GTG GGC Pro Thr Pro Val Met Ala Asp Glu Arg Glu Pro Ile Ala Ile Val Gly 2630 2635 2640			8275
50	ATG GCG TGC CGT TAC CCG GGC GGT GTG GCG TCG CCG GAC GAC CTG TCG Met Ala Cys Arg Tyr Pro Gly Gly Val Ala Ser Pro Asp Asp Leu Trp 2645 2650 2655			8323
55	GAC CTG GTG GCC GGT GAC GGG CAC ACG CTC TCC CCG TTC CCG GCC GAC Asp Leu Val Ala Gly Asp Gly His Thr Leu Ser Pro Phe Pro Ala Asp			8371

EP 0 791 655 A2

	2660	2665	2670	
5	CGT GGC TGG GAC GTC Arg Gly Trp Asp Val 2675	GAG GGG CTG TAC GAC Glu Gly Leu Tyr Asp 2680	CCG GAG CCG GGG GTG CCG Pro Glu Pro Gly Val Pro 2685	8419
	GGC AAG AGC TAT GTA CGG GAA GGC GGG TTC CTG CGT TCC GCG GCC GAG Gly Lys Ser Tyr Val Arg Glu Gly Gly Phe Leu Arg Ser Ala Ala Glu 2695		2700	8467
10	TTC GAC GCG GAG TTC TTC GGG ATA TCG CCG CGC GAG GCC ACG GCC ATG Phe Asp Ala Glu Phe Phe Gly Ile Ser Pro Arg Glu Ala Thr Ala Met 2710		2715	8515
15	GAC CCG CAG CAG CCG TTG CTG CTG GAG ACG TCG TGG GAG GCG CTG GAG Asp Pro Gln Gln Arg Leu Leu Leu Glu Thr Ser Trp Glu Ala Leu Glu 2725		2730	8563
20	CGG GCC GGC ATC GTT CCG GAC TCG CTG CGC GGC ACC CCG ACC GGT GTC Arg Ala Gly Ile Val Pro Asp Ser Leu Arg Gly Thr Arg Thr Gly Val 2740		2745	8611
	TTC AGC GGC ATC TCC CAG CAG GAC TAC GCG ACC CAG CTG GGG GAC GCC Phe Ser Gly Ile Ser Gln Gln Asp Tyr Ala Thr Gln Leu Gly Asp Ala 2755		2760	8659
25	GCC GAC ACC TAC GGC GGG CAT GTG CTC ACG GGG ACC CTC GGC AGT GTG Ala Asp Thr Tyr Gly Gly His Val Leu Thr Gly Thr Leu Gly Ser Val 2775		2780	8707
30	ATC TCC GGT CCG GTT GCC TAT GCG TTG GGG TTG GAG GGG CCG GCG CTG Ile Ser Gly Arg Val Ala Tyr Ala Leu Gly Leu Glu Gly Pro Ala Leu 2790		2795	8755
35	ACG GTG GAC ACG GCG TGT TCG TCG TCG TTG GTG GCG TTG CAT CTG GCG Thr Val Asp Thr Ala Cys Ser Ser Ser Leu Val Ala Leu His Leu Ala 2805		2810	8803
	GTG CAG TCG TTG CCG CCG GGT GAG TGT GAT CTG GCG TTG GCC GGT GCG Val Gln Ser Leu Arg Arg Gly Glu Cys Asp Leu Ala Leu Ala Gly Gly 2820		2825	8851
40	GTG ACG GTG ATG GCG ACG CCG ACG GTG TTC GTG GAG TTC TCG CCG CAG Val Thr Val Met Ala Thr Pro Thr Val Phe Val Glu Phe Ser Arg Gln 2835		2840	8899
45	CGG GGG CTG GCG GCG GAC GGG CCG TGC AAG GCG TTC GCG GAG GGT GCG Arg Gly Leu Ala Ala Asp Gly Arg Cys Lys Ala Phe Ala Glu Gly Ala 2855		2860	8947
50	GAC GGG ACG GCG TGG CCG GAG GGT GTG GGT GTG CTG CTG GTG GAG CCG Asp Gly Thr Ala Trp Ala Glu Gly Val Gly Val Leu Leu Val Glu Arg 2870		2875	8995
	CTT TCC GAC GCG CCG CCG AAC GGT CAT CCG CTG CTG CCG CTG GTG CCG Leu Ser Asp Ala Arg Arg Asn Gly His Arg Val Leu Ala Val Val Arg 2885		2890	9043
55	GCG AGT GCG GTC AAT CAG GAC GGT GCG AGC AAT GGG CTG ACG GCG CCG Gly Ser Ala Val Asn Gln Asp Gly Ala Ser Asn Gly Leu Thr Ala Pro			9091

EP 0 791 655 A2

	2900	2905	2910	
5	AGT GGT CCG GCG CAG CAG CCG GTG ATC CGT GAG GCG CTG GCT GAT GCG Ser Gly Pro Ala Gln Gln Arg Val Ile Arg Glu Ala Leu Ala Asp Ala 2915 2920 2925 2930			9139
	GGG CTG GTG CCC GCC GAC GTG GAT GTG GTG GAG GCG CAC GGT ACG GCG Gly Leu Val Pro Ala Asp Val Asp Val Val Glu Ala His Gly Thr Gly 2935 2940 2945			9187
10	ACG GCG CTG GGT GAT CCG ATC GAG GCG GGT GCG CTG CTG GCC ACG TAC Thr Ala Leu Gly Asp Pro Ile Glu Ala Gly Ala Leu Leu Ala Thr Tyr 2950 2955 2960			9235
15	GGG CCG GAG CCG GTC GGC GAT CCG TTG TGG CTC GGG TCG TTG AAG TCG Gly Arg Glu Arg Val Gly Asp Pro Leu Trp Leu Gly Ser Leu Lys Ser 2965 2970 2975			9283
20	AAC ATC GGG CAT GCG CAG GCG GCT GCG GGT GTG GGT GGT GTG ATC AAG Asn Ile Gly His Ala Gln Ala Ala Ala Gly Val Gly Gly Val Ile Lys 2980 2985 2990			9331
	GTG GTG CAG GGG ATG CCG CAT GGG TCG TTG CCG CCG ACG CTG CAT GTG Val Val Gln Gly Met Arg His Gly Ser Leu Pro Arg Thr Leu His Val 2995 3000 3005 3010			9379
25	GAT GCG CCG TCG TCG AAG GTG GAG TCG GCT TCG GGT CCG GTG GAG CTG Asp Ala Pro Ser Ser Lys Val Glu Trp Ala Ser Gly Ala Val Glu Leu 3015 3020 3025			9427
30	CTG ACC GAG ACC CCG TCG TGG CCG CCG CCG GTG GAG CCG GTG CCG CCG Leu Thr Glu Thr Arg Ser Trp Pro Arg Arg Val Glu Arg Val Arg Arg 3030 3035 3040			9475
35	GCC GCG GTG TCG GCG TTC GGG GTG AGC GGG ACC AAC GCC CAT GTG GTC Ala Ala Val Ser Ala Phe Gly Val Ser Gly Thr Asn Ala His Val Val 3045 3050 3055			9523
	CTG GAG GAA CCG CCG GCG GAG GCC GGG ACC GAG CAC GGG GAC GGC CCT Leu Glu Glu Ala Pro Ala Glu Ala Gly Ser Glu His Gly Asp Gly Pro 3060 3065 3070			9571
40	GAA CCT GAG CCG CCC GAC GCG GTG ACG GGT CCG TTG TCG TGG GTG CTT Glu Pro Glu Arg Pro Asp Ala Val Thr Gly Pro Leu Ser Trp Val Leu 3075 3080 3085 3090			9619
45	TCT CCG CCG TCG GAG GGG GCG TTG CCG GCG CAG GCG GTG CCG TTG CGT Ser Ala Arg Ser Glu Gly Ala Leu Arg Ala Gln Ala Val Arg Leu Arg 3095 3100 3105			9667
	GAG TGT GTG GAG CCG GTG GGT GCG GAT CCG CCG GAT GTG CCG GGG TCG Glu Cys Val Glu Arg Val Gly Ala Asp Pro Arg Asp Val Ala Gly Ser 3110 3115 3120			9715
50	TTG GTG GTG TCG CGT GCG TCG TTC GGT GAG CGT CCG GTG GTG GTG GGC Leu Val Val Ser Arg Ala Ser Phe Gly Glu Arg Ala Val Val Val Gly 3125 3130 3135			9763
55	CGG GGG CGT GAG GAG TTG CTG GCG GGT CTG GAT GTG GTG GCT GCC GGG Arg Gly Arg Glu Glu Leu Leu Ala Gly Leu Asp Val Val Ala Ala Gly			9811

EP 0 791 655 A2

	3140	3145	3150	
5	GCT CCT GTG GGT GTG TCT TCG GGG GCC GGT GCT GTG GTG CCG GGG AGT Ala Pro Val Gly Val Ser Ser Gly Ala Gly Ala Val Val Arg Gly Ser 3155 3160 3165 3170			9859
	CGC GTG CCG GGT CGT GGG GTG GGG GTG TTG TTC ACG GGT CAG GGT GCG Ala Val Arg Gly Arg Gly Val Gly Val Leu Phe Thr Gly Gln Gly Ala 3175 3180 3185			9907
10	CAG TGG GTT GGT ATG GGG CGT GGG TTG TAT GCG GGG GGT GGG GTG TTT Gln Trp Val Gly Met Gly Arg Gly Leu Tyr Ala Gly Gly Gly Val Phe 3190 3195 3200			9955
15	CGC GAG GTG CTG GAT GAG GTG TTG TCG GTG GTG GGG GAG GTG GAT GGT Ala Glu Val Leu Asp Glu Val Leu Ser Val Val Gly Glu Val Asp Gly 3205 3210 3215			10003
20	CGG TCG TTG CCG GAT GTG ATG TTC GCG GAT GCT GAC TCG GTT TTG GGT Arg Ser Leu Arg Asp Val Met Phe Ala Asp Ala Asp Ser Val Leu Gly 3220 3225 3230			10051
	GGG TTG TTG GGT CCG ACG GAG TTT GCT CAG CCT GCG TTG TTT CCG TTG Gly Leu Leu Gly Arg Thr Glu Phe Ala Gln Pro Ala Leu Phe Ala Leu 3235 3240 3245 3250			10099
25	GAG GTG GCG TTG TTC CCG GCG TTG GAG GCT CCG GGT GTG CAG GTG TCG Glu Val Ala Leu Phe Arg Ala Leu Glu Ala Arg Gly Val Glu Val Ser 3255 3260 3265			10147
30	GTG GTG TTG GGT CAT TCG GTG GCG GAG GTG GCT GCT GCG TAT GTG GCG Val Val Leu Gly His Ser Val Gly Glu Val Ala Ala Ala Tyr Val Ala 3270 3275 3280			10195
35	GGG GTG TTG TCG TTG GGT GAT GCG GTG CCG TTG GTG GTG GCG CCG GGT Gly Val Leu Ser Leu Gly Asp Ala Val Arg Leu Val Val Ala Arg Gly 3285 3290 3295			10243
	GGG TTG ATG GGT GGG TTG CCG GTG GGT GGG GGG ATG TCG TCG GTG GGG Gly Leu Met Gly Gly Leu Pro Val Gly Gly Gly Met Trp Ser Val Gly 3300 3305 3310			10291
40	GCG TCG GAG TCG GTG GTG CCG GGG GTT GTT GAG GGG TTG GGG GAG TCG Ala Ser Glu Ser Val Val Arg Gly Val Val Glu Gly Leu Gly Glu Trp 3315 3320 3325 3330			10339
45	GTG TCG GTT GCG GCG GTG AAT GGG CCG CCG TCG GTG GTG TTG TCG GGT Val Ser Val Ala Ala Val Asn Gly Pro Arg Ser Val Val Leu Ser Gly 3335 3340 3345			10387
	GAT GTG GGT GTG CTG GAG TCG GTG GTT GTC ACG CTG ATG GGG GAT GGG Asp Val Gly Val Leu Glu Ser Val Val Val Thr Leu Met Gly Asp Gly 3350 3355 3360			10435
50	GTG GAG TGC CCG CCG TTG GAT GTG TCG CAT GGG TTT CAT TCG GTG TTG Val Glu Cys Arg Arg Leu Asp Val Ser His Gly Phe His Ser Val Leu 3365 3370 3375			10483
55	ATG GAG CCG GTG TTG GGG GAG TTC CCG GGG GTT GTG GAG TCG TTG GAG Met Glu Pro Val Leu Gly Glu Phe Arg Gly Val Val Glu Ser Leu Glu			10531

EP 0 791 655 A2

	3380	3385	3390	
5	TTC GGT CGG GTG CGG CCG GGT GTG GTG GTG TCG GGT GTG TCG GGT Phe Gly Arg Val Arg Pro Gly Val Val Val Val Ser Gly Val Ser Gly 3395 3400 3405 3410	10579		
10	GGG GTG GTG GGT TCG GGG GAG TTG GGG GAT CCG GGG TAT TGG GTG CGT Gly Val Val Gly Ser Gly Glu Leu Gly Asp Pro Gly Tyr Trp Val Arg 3415 3420 3425	10627		
15	CAT GCG CGG GAG GCG GTG CGT TTC GCG GAT GGG GTG GGG GTG GTG CGT His Ala Arg Glu Ala Val Arg Phe Ala Asp Gly Val Gly Val Val Arg 3430 3435 3440	10675		
20	GGT CTG GGT GTG GGG ACG TTG GTG GAG GTG GGT CCG CAT GGG GTG CTG Gly Leu Gly Val Gly Thr Leu Val Glu Val Gly Pro His Gly Val Leu 3445 3450 3455	10723		
25	ACG GGG ATG GCG GGT CAG TGC CTG GAG GCC GGT GAT GAT GTG GTG GTG Thr Gly Met Ala Gly Gln Cys Leu Glu Ala Gly Asp Asp Val Val Val 3460 3465 3470	10771		
30	GTG CCG GCG ATG CCG CCG GGC CGT CCG GAG CCG GAG GTG TTC GAG GCG Val Pro Ala Met Arg Arg Gly Arg Pro Glu Arg Glu Val Phe Glu Ala 3475 3480 3485 3490	10819		
35	GCG CTG GCG ACG GTG TTC ACC CCG GAC GCC GGC CTC GAC GCC ACG ACA Ala Leu Ala Thr Val Phe Thr Arg Asp Ala Gly Leu Asp Ala Thr Thr 3495 3500 3505	10867		
40	CTC CAC ACC GGG AGC ACC GGC CGA CGC ATC GAC CTC CCC ACC TAC CCC Leu His Thr Gly Ser Thr Gly Arg Arg Ile Asp Leu Pro Thr Tyr Pro 3510 3515 3520	10915		
45	TTC CAA CAC AAC CGC TAC TGG GCA ACC GGC TCA GTG ACC GGT GCG ACC Phe Gln His Asn Arg Tyr Trp Ala Thr Gly Ser Val Thr Gly Ala Thr 3525 3530 3535	10963		
50	GGC ACC TCG GCA GCC GCG CGC TTC GGC CTG GAG TGG AAG GAC CAC CCC Gly Thr Ser Ala Ala Ala Arg Phe Gly Leu Glu Trp Lys Asp His Pro 3540 3545 3550	11011		
55	TTC CTC ACC GGC GCC ACG CCG ATA GCC GGC TCC GGC GCG CTG CTC CTC Phe Leu Ser Gly Ala Thr Pro Ile Ala Gly Ser Gly Ala Leu Leu Leu 3555 3560 3565 3570	11059		
60	ACC GGC AGG GTG GGG CTC GCT GCC CAC CCG TGG CTG GCC GAC CAC GCC Thr Gly Arg Val Gly Leu Ala Ala His Pro Trp Leu Ala Asp His Ala 3575 3580 3585	11107		
65	ATC TCC GGC ACG GTG CTG CTC CCC GGA ACG GCG ATC GCC GAC CTG CTG Ile Ser Gly Thr Val Leu Leu Pro Gly Thr Ala Ile Ala Asp Leu Leu 3590 3595 3600	11155		
70	CTG CCG GCG GTC GAG GAG GTC GCC GCC GGA GGG GTC GAG GAA CTG ACG Leu Arg Ala Val Glu Glu Val Gly Ala Gly Gly Val Glu Glu Leu Thr 3605 3610 3615	11203		
75	CTC CAT GAG CCC CTG CTC CTC CCC GAG CGA GGC GGC CTG CAC GTC CAG Leu His Glu Pro Leu Leu Leu Pro Glu Arg Gly Gly Leu His Val Gln	11251		

EP 0 791 655 A2

	3620	3625	3630	
5	GTG CTG GTC GAG GCG GCC GAC GAG CAG GGA CGG CGT GCC GTG GCA GTC Val Leu Val Glu Ala Ala Asp Glu Gln Gly Arg Arg Ala Val Ala Val 3635 3640 3645 3650			11299
10	GCC GCA CGC CCG GAG GGC CCT GGG CGG GAC GGT GAG GAA CAG GAG TGG Ala Ala Arg Pro Glu Gly Pro Gly Arg Asp Gly Glu Glu Gln Glu Trp 3655 3660 3665			11347
15	ACC CGG CAC GCG GAA GGC GTG CTC ACC TCC ACC GAG ACG GCC GTT CCG Thr Arg His Ala Glu Gly Val Leu Thr Ser Thr Glu Thr Ala Val Pro 3670 3675 3680			11395
20	GAC ATG GGC TGG GCC GCC GGG GCC TGG CCG CCG CCC GGT GCC GAG CCG Asp Met Gly Trp Ala Ala Gly Ala Trp Pro Pro Pro Gly Ala Glu Pro 3685 3690 3695			11443
25	ATC GAC GTC GAG GAG CTG TAC GAC GCG TTC GCC GCG GAC GGC TAC GGC Ile Asp Val Glu Glu Leu Tyr Asp Ala Phe Ala Ala Asp Gly Tyr Gly 3700 3705 3710			11491
30	TAC GGC CCG GCC TTC ACC GCA CTG TCC GGC GTG TGG CGT CTC GGC GAC Tyr Gly Pro Ala Phe Thr Ala Leu Ser Gly Val Trp Arg Leu Gly Asp 3715 3720 3725 3730			11539
35	GAA CTC TTC GCC GAG GTG CGG CGG CCC GCG GGC GGC GCG GGC ACG ACC Glu Leu Phe Ala Glu Val Arg Arg Pro Ala Gly Gly Ala Gly Thr Thr 3735 3740 3745			11587
40	GGT GAC GGT TTC GGC GTC CAC CCC GCA CTC TTC GAT GCG GCC CTC CAC Gly Asp Gly Phe Gly Val His Pro Ala Leu Phe Asp Ala Ala Leu His 3750 3755 3760			11635
45	CCG TGG CGC GCC GGC GGG CTG CTG CCC GAC ACG GGC GGC ACC ACC TGG Pro Trp Arg Ala Gly Gly Leu Leu Pro Asp Thr Gly Gly Thr Thr Trp 3765 3770 3775			11683
50	GCG CCG TTC TCC TGG CAG GGC ATC GCG CTC CAC ACC ACC GGA GCC GAG Ala Pro Phe Ser Trp Gln Gly Ile Ala Leu His Thr Thr Gly Ala Glu 3780 3785 3790			11731
55	ACG CTC CGC GTC AGA CTG GCC CCT GCG GCC GGC GGC ACC GAG TCG GCC Thr Leu Arg Val Arg Leu Ala Pro Ala Ala Gly Gly Thr Glu Ser Ala 3795 3800 3805 3810			11779
60	TTC TCC GTA CAG GCC GCC GAC CCG GCG GGC ACC CCG GTC CTC ACC CTC Phe Ser Val Gln Ala Ala Asp Pro Ala Gly Thr Pro Val Leu Thr Leu 3815 3820 3825			11827
65	GAC GCA CTG CTG CTC CGC CCG GTG ACC CTG GGG AGG GCC GAC GCG CCG Asp Ala Leu Leu Leu Arg Pro Val Thr Leu Gly Arg Ala Asp Ala Pro 3830 3835 3840			11875
70	CAA CCG CTG TAC CGC GTC GAC TGG CAG CCG GTC GGC CAG GGG ACC GAG Gln Pro Leu Tyr Arg Val Asp Trp Gln Pro Val Gly Gln Gly Thr Glu 3845 3850 3855			11923
75	GCC TCC GGC GCC CAG GGC TGG ACG GTG CTC GGG CAG GCC GCG GCC GAG Ala Ser Gly Ala Gln Gly Trp Thr Val Leu Gly Gln Ala Ala Ala Glu			11971

EP 0 791 655 A2

	3860	3865	3870	
5	ACG GTC GCG CAG CCC GCC GCC CAT GCG GAC CTC ACC GCC CTG CGT ACG Thr Val Ala Gln Pro Ala Ala His Ala Asp Leu Thr Ala Leu Arg Thr 3875 3880 3885 3890	12019		
10	GCT GTG GCC GCG GCG GGA ACA CCC GTG CCC CGG CTG GTG GTC GTG TCG Ala Val Ala Ala Ala Gly Thr Pro Val Pro Arg Leu Val Val Val Ser 3895 3900 3905	12067		
15	CCG GTG GAC ACC CGG CTG GAC GAG GGG CCG GTG CTG GCG GAC GCC GAG Pro Val Asp Thr Arg Leu Asp Glu Gly Pro Val Leu Ala Asp Ala Glu 3910 3915 3920	12115		
20	GCT CGG GCC CGT GCG GGT GAC GGC TGG GAC GAC GAT CCC CTA CGT GTC Ala Arg Ala Arg Ala Gly Asp Gly Trp Asp Asp Pro Leu Arg Val 3925 3930 3935	12163		
25	GCC CTC GGG CCG GGC CTG ACC CTG GTC CCG GAG TGG GTC GAG GAC GAA Ala Leu Gly Arg Gly Leu Thr Leu Val Arg Glu Trp Val Glu Asp Glu 3940 3945 3950	12211		
30	CGG TTG GCG GAC TCC CGG CTC GTC GTC CTC ACC CGT GGC GCG GTG GCG Arg Leu Ala Asp Ser Arg Leu Val Val Leu Thr Arg Gly Ala Val Ala 3955 3960 3965 3970	12259		
35	GCC GGT CCC GGC GAT GTG CCG GAC CTG ACA GGT GCG GCC CTG TGG GGG Ala Gly Pro Gly Asp Val Pro Asp Leu Thr Gly Ala Ala Leu Trp Gly 3975 3980 3985	12307		
40	CTG CTC CGC TCC GCG CAG TCG GAG TAT CCG GAC CGC TTC ACC CTC ATC Leu Leu Arg Ser Ala Gln Ser Glu Tyr Pro Asp Arg Phe Thr Leu Ile 3990 3995 4000	12355		
45	GAC GTG GAC GAT TCC CCC GAG TCC CGT GCG GCT CTG CCC CGG GCT CTG Asp Val Asp Asp Ser Pro Glu Ser Arg Ala Ala Leu Pro Arg Ala Leu 4005 4010 4015	12403		
50	GGA TCG GCC GAG CGA CAA CTC GCC CTG CCG ACC GGC GAC GTG CTG GCG Gly Ser Ala Glu Arg Gln Leu Ala Leu Arg Thr Gly Asp Val Leu Ala 4020 4025 4030	12451		
55	CCG GCC CTG GTC CCG ATG GCC ACC CCG CCG GCG GAG ACC ACT CCA GCG Pro Ala Leu Val Pro Met Ala Thr Arg Pro Ala Glu Thr Thr Pro Ala 4035 4040 4045 4050	12499		
60	ACG GCG GTC GCC TCG GCG ACA ACA CAG ACA CAG GTC ACC GCG CCC GCT Thr Ala Val Ala Ser Ala Thr Thr Gln Thr Gln Val Thr Ala Pro Ala 4055 4060 4065	12547		
65	CCC GAC GAC CCG GCT GCG GAT GCC GTG TTC GAC CCG GCG GGC ACC GTA Pro Asp Asp Pro Ala Ala Asp Ala Val Phe Asp Pro Ala Gly Thr Val 4070 4075 4080	12595		
70	CTG ATC ACC GGC GGC ACC GGC GCC CTG GGA CCG CGT GTC GCC TCG CAC Leu Ile Thr Gly Gly Thr Gly Ala Leu Gly Arg Arg Val Ala Ser His 4085 4090 4095	12643		
75	CTC GCG CGC CGG TAC GGC GTA CGC CAC ATG CTT CTG GTC AGC AGG CGT Leu Ala Arg Arg Tyr Gly Val Arg His Met Leu Leu Val Ser Arg Arg	12691		

EP 0 791 655 A2

	4100	4105	4110	
5	GGA CCG GAC GCC CCC GAG GCC GGT CCC CTG GAA CGG GAA CTC GCC GGT Gly Pro Asp Ala Pro Glu Ala Gly Pro Leu Glu Arg Glu Leu Ala Gly 4115 4120 4125 4130	12739		
10	CTC GGA GTC ACC GCC ACC TTC CTG GCA TGC GAC CTC ACC GAC ATC GAG Leu Gly Val Thr Ala Thr Phe Leu Ala Cys Asp Leu Thr Asp Ile Glu 4135 4140 4145	12787		
15	GCC GTA CGG AAG GCC GTC GCC GCG GTG CCG TCG GAC CAC CCG CTG ACC Ala Val Arg Lys Ala Val Ala Ala Val Pro Ser Asp His Pro Leu Thr 4150 4155 4160	12835		
20	GGT GTG GTG CAC ACC GCC GGC GTG CTG GAC GAC GGC GCC CTG ACC GGC Gly Val Val His Thr Ala Gly Val Leu Asp Asp Gly Ala Leu Thr Gly 4165 4170 4175	12883		
25	CTG ACC CGG CAA CGC CTC GAC ACC GTG CTG CGG CCC AAG GCC GAC GCC Leu Thr Arg Gln Arg Leu Asp Thr Val Leu Arg Pro Lys Ala Asp Ala 4180 4185 4190	12931		
30	GTG CGG AAC CTC CAC GAG GCG ACC CTC GAC CGG CCG CTG CGC GCG TTC Val Arg Asn Leu His Glu Ala Thr Leu Asp Arg Pro Leu Arg Ala Phe 4195 4200 4205 4210	12979		
35	GTC CTG TTC TCC GCC GCC GCC GGA CTC CTG GGC CGC CCC GGG CAG GCC Val Leu Phe Ser Ala Ala Ala Gly Leu Leu Gly Arg Pro Gly Gln Ala 4215 4220 4225	13027		
40	TCC TAC GCC GCC GCC AAC GCG GTC CTC GAC GCG CTC GCG GGA GCC CGC Ser Tyr Ala Ala Ala Asn Ala Val Leu Asp Ala Leu Ala Gly Ala Arg 4230 4235 4240	13075		
45	CGC GCG GCC GGA CTG CCC GCA GTG TCC CTG GCG TGG GGC CTG TGG GAC Arg Ala Ala Gly Leu Pro Ala Val Ser Leu Ala Trp Gly Leu Trp Asp 4245 4250 4255	13123		
50	GAG CAG ACG GGC ATG GCA GGA GGC CTC GAC GAG ATG GCC CTG CGC GTG Glu Gln Thr Gly Met Ala Gly Gly Leu Asp Glu Met Ala Leu Arg Val 4260 4265 4270	13171		
55	CTG CGC CGG GAC GGC ATC GCC GCG ATG CCT CCG GAG CAG GGG CTC GAA Leu Arg Arg Asp Gly Ile Ala Ala Met Pro Pro Glu Gln Gly Leu Glu 4275 4280 4285 4290	13219		
60	CTG CTC GAC CTG GCC CTG ACC GGA CAC CGG GAC GGA CCC GCC CTC CTC Leu Leu Asp Leu Ala Leu Thr Gly His Arg Asp Gly Pro Ala Val Leu 4295 4300 4305	13267		
65	GTC CCC CTC CTC CTC GAC GGC GCG GCC CTG CGC CGC ACG GCG AAG GAG Val Pro Leu Leu Leu Asp Gly Ala Ala Leu Arg Arg Thr Ala Lys Glu 4310 4315 4320	13315		
70	CGC GGC GCG GCC ACG ATG TCC CCC TTG CTG CGC GCC CTG CTG CCC GCC Arg Gly Ala Ala Thr Met Ser Pro Leu Leu Arg Ala Leu Leu Pro Ala 4325 4330 4335	13363		
75	GCC CTG CGC CGC AGC GGT GGA GCC GGC GCC CCC GCG GCG GCC GAC CGG Ala Leu Arg Arg Ser Gly Gly Ala Gly Ala Pro Ala Ala Ala Asp Arg 4340 4345 4350	13411		

	4340	4345	4350	
5	CAC GGC AAG GAG GCG GAC CCC GGT GCG GGA CGC CTC GCA GGG ATG GTG His Gly Lys Glu Ala Asp Pro Gly Ala Gly Arg Leu Ala Gly Met Val 4355	4360	4365	13459 4370
10	GCA CTC GAA GCG GCG GAG CGT TCC GCG GCC GTC CTT GAG CTG GTC ACC Ala Leu Glu Ala Ala Glu Arg Ser Ala Ala Val Leu Glu Leu Val Thr 4375	4380	4385	13507
15	GAA CAG GTC GCC GAG GTC CTC GGC TAC GCG TCG GCC GCG GAG ATC GAG Glu Gln Val Ala Glu Val Leu Gly Tyr Ala Ser Ala Ala Glu Ile Glu 4390	4395	4400	13555
20	CCC GAA CGA CCC TTC CGG GAG ATC GGC GTC GAC TCC CTG GCG GCG GTG Pro Glu Arg Pro Phe Arg Glu Ile Gly Val Asp Ser Leu Ala Ala Val 4405	4410	4415	13603
25	GAG CTG CGC AAC CGG CTC ACC CGT CTG GTC GCC CTG CGG TTG CCG ACC Glu Leu Arg Asn Arg Leu Ser Arg Leu Val Gly Leu Arg Leu Pro Thr 4420	4425	4430	13651
30	ACG CTG TCC TTC GAC CAC CCC ACG CCG AAG GAC ATG GCG CAG CAC ATC Thr Leu Ser Phe Asp His Pro Thr Pro Lys Asp Met Ala Gln His Ile 4435	4440	4445	13699 4450
35	GAC GGG CAG CTC CCC CGC CCG GCC GGA GCC TCG CCC GCG GAC GCA GCG Asp Gly Gln Leu Pro Arg Pro Ala Gly Ala Ser Pro Ala Asp Ala Ala 4455	4460	4465	13747
40	CTG GAA GGG ATC GGC GAC CTC GCG CGG GCG GTC GCC CTG CTG GGC ACG Leu Glu Gly Ile Gly Asp Leu Ala Arg Ala Val Ala Leu Leu Gly Thr 4470	4475	4480	13795
45	GGC GAC GCC CGC CGG GCC GAG GTA CGA GAG CAG CTC GTC GGA CTG CTG Gly Asp Ala Arg Arg Ala Glu Val Arg Glu Gln Leu Val Gly Leu Leu 4485	4490	4495	13843
50	GCC GCG CTC GAC CCA CCT GGG CGG ACG GGC ACC GCC GCA CCC GGC GTC Ala Ala Leu Asp Pro Pro Gly Arg Thr Gly Thr Ala Ala Pro Gly Val 4500	4505	4510	13891
55	CCC TCC GGT GCC GAT GGC GCG GAA CCG ACC GTG ACG GAC CGG CTC GAC Pro Ser Gly Ala Asp Gly Ala Glu Pro Thr Val Thr Asp Arg Leu Asp 4515	4520	4525	13939 4530
60	GAG GCG ACC GAC GAC GAG ATC TTC GCC TTC CTG GAC GAG CAG CTG TGA Glu Ala Thr Asp Asp Glu Ile Phe Ala Phe Leu Asp Glu Gln Leu *	4535	4540	13987 4545

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4546 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

5 Met Ser Gly Glu Leu Ala Ile Ser Arg Ser Asp Asp Arg Ser Asp Ala
 1 5 10 15
 Val Ala Val Val Gly Met Ala Cys Arg Phe Pro Gly Ala Pro Gly Ile
 20 25 30
 10 Ala Glu Phe Trp Glu Leu Leu Arg Ser Gly Arg Gly Met Pro Thr Arg
 35 40 45
 Gln Asp Asp Gly Thr Trp Arg Ala Ala Leu Glu Asp His Ala Gly Phe
 50 55 60
 15 Asp Ala Gly Phe Phe Gly Met Asn Ala Arg Gln Ala Ala Ala Thr Asp
 65 70 75 80
 Pro Gln His Arg Leu Met Leu Glu Leu Gly Trp Glu Ala Leu Glu Asp
 85 90 95
 20 Ala Gly Ile Val Pro Gly Asp Leu Thr Gly Thr Asp Thr Gly Val Phe
 100 105 110
 Ala Gly Val Ala Ser Asp Asp Tyr Ala Val Leu Thr Arg Arg Ser Ala
 115 120 125
 25 Val Ser Ala Gly Gly Tyr Thr Ala Thr Gly Leu His Arg Ala Leu Ala
 130 135 140
 Ala Asn Arg Leu Ser His Phe Leu Gly Leu Arg Gly Pro Ser Leu Val
 145 150 155 160
 30 Val Asp Ser Ala Gln Ser Ala Ser Leu Val Ala Val Gln Leu Ala Cys
 165 170 175
 Glu Ser Leu Arg Arg Gly Glu Thr Ser Leu Ala Val Ala Gly Gly Val
 180 185 190
 35 Asn Leu Ile Leu Thr Glu Glu Ser Thr Thr Val Met Glu Arg Met Gly
 195 200 205
 Ala Leu Ser Pro Asp Gly Arg Cys His Thr Phe Asp Ala Arg Ala Asn
 210 215 220
 40 Gly Tyr Val Arg Gly Glu Gly Gly Gly Ala Val Val Leu Lys Pro Leu
 225 230 235 240
 45 Asp Ala Ala Leu Ala Asp Gly Asp Arg Val Tyr Cys Val Ile Lys Gly
 245 250 255
 Gly Ala Val Asn Asn Asp Gly Gly Gly Ala Ser Leu Thr Thr Pro Asp
 260 265 270
 50 Arg Glu Ala Gln Glu Ala Val Leu Arg Gln Ala Tyr Arg Arg Ala Gly
 275 280 285
 Val Ser Thr Gly Ala Val Arg Tyr Val Glu Leu His Gly Thr Gly Thr
 290 295 300
 55 Arg Ala Gly Asp Pro Val Glu Ala Ala Ala Leu Gly Ala Val Leu Gly

EP 0 791 655 A2

	305		310		315		320
	Ala Gly Ala Asp Ser Gly Arg Ser Thr Pro Leu Ala Val Gly Ser Val						
		325			330		335
5	Lys Thr Asn Val Gly His Leu Glu Gly Ala Ala Gly Ile Val Gly Leu						
		340		345			350
	Ile Lys Ala Thr Leu Cys Val Arg Lys Gly Glu Leu Val Pro Ser Leu						
10		355		360			365
	Asn Phe Ser Thr Pro Asn Pro Asp Ile Pro Leu Asp Asp Leu Arg Leu						
		370		375			380
	Arg Val Gln Thr Glu Arg Gln Glu Trp Asn Glu Glu Asp Asp Arg Pro						
15		385		390		395	400
	Arg Val Ala Gly Val Ser Ser Phe Gly Met Gly Gly Thr Asn Val His						
		405		410			415
	Leu Val Ile Ala Glu Ala Pro Ala Ala Ala Gly Ser Ser Gly Ala Gly						
20		420		425			430
	Gly Ser Gly Ala Gly Ser Gly Ala Gly Ile Ser Ala Val Ser Gly Val						
		435		440			445
	Val Pro Val Val Val Ser Gly Arg Ser Arg Val Val Val Arg Glu Ala						
25		450		455			460
	Ala Gly Arg Leu Ala Glu Val Val Glu Ala Gly Gly Val Gly Leu Ala						
		465		470		475	480
30	Asp Val Ala Val Thr Met Ala Asp Arg Ser Arg Phe Gly Tyr Arg Ala						
		485		490			495
	Val Val Leu Ala Arg Gly Glu Ala Glu Leu Ala Gly Arg Leu Arg Ala						
35		500		505			510
	Leu Ala Gly Gly Asp Pro Asp Ala Gly Val Val Thr Gly Ala Val Leu						
		515		520			525
	Asp Gly Gly Val Val Val Gly Ala Ala Pro Gly Gly Ala Gly Ala Ala						
40		530		535		540	
	Gly Gly Ala Gly Ala Ala Gly Gly Ala Gly Gly Gly Gly Val Val Leu						
		545		550		555	560
	Val Phe Pro Gly Gln Gly Thr Gln Trp Val Gly Met Gly Ala Gly Leu						
45		565		570			575
	Leu Gly Ser Ser Glu Val Phe Ala Ala Ser Met Arg Glu Cys Ala Arg						
		580		585			590
	Ala Leu Ser Val His Val Gly Trp Asp Leu Leu Glu Val Val Ser Gly						
50		595		600			605
	Gly Ala Gly Leu Glu Arg Val Asp Val Val Gln Pro Val Thr Trp Ala						
		610		615			620
55	Val Met Val Ser Leu Ala Arg Tyr Trp Gln Ala Met Gly Val Asp Val						

EP 0 791 655 A2

	625		630		635		640
	Ala Ala Val Val Gly His Ser Gln Gly Glu Ile Ala Ala Ala Thr Val						
5			645		650		655
	Ala Gly Ala Leu Ser Leu Glu Asp Ala Ala Ala Val Val Ala Leu Arg						
			660		665		670
10	Ala Gly Leu Ile Gly Arg Tyr Leu Ala Gly Arg Gly Ala Met Ala Ala						
			675		680		685
	Val Pro Leu Pro Ala Gly Glu Val Glu Ala Gly Leu Ala Lys Trp Pro						
			690		695		700
15	Gly Val Glu Val Ala Ala Val Asn Gly Pro Ala Ser Thr Val Val Ser						
			705		710		715
	Gly Asp Arg Arg Ala Val Ala Gly Tyr Val Ala Val Cys Gln Ala Glu						
			725		730		735
20	Gly Val Gln Ala Arg Leu Ile Pro Val Asp Tyr Ala Ser His Ser Arg						
			740		745		750
	His Val Glu Asp Leu Lys Gly Glu Leu Glu Arg Val Leu Ser Gly Ile						
			755		760		765
25	Arg Pro Arg Ser Pro Arg Val Pro Val Cys Ser Thr Val Ala Gly Glu						
			770		775		780
	Gln Pro Gly Glu Pro Val Phe Asp Ala Gly Tyr Trp Phe Arg Asn Leu						
			785		790		795
30	Arg Asn Arg Val Glu Phe Ser Ala Val Val Gly Gly Leu Leu Glu Glu						
			805		810		815
	Gly His Arg Arg Phe Ile Glu Val Ser Ala His Pro Val Leu Val His						
			820		825		830
35	Ala Ile Glu Gln Thr Ala Glu Ala Ala Asp Arg Ser Val His Ala Thr						
			835		840		845
	Gly Thr Leu Arg Arg Gln Asp Asp Ser Pro His Arg Leu Leu Thr Ser						
40			850		855		860
	Thr Ala Glu Ala Trp Ala His Gly Ala Thr Leu Thr Trp Asp Pro Ala						
			865		870		875
	Leu Pro Pro Gly His Leu Thr Thr Leu Pro Thr Tyr Pro Phe Asn His						
45			885		890		895
	His His Tyr Trp Leu Asp Thr Ile Asp Gly Gly Gly Gly Asp Asp Ala						
			900		905		910
50	Thr Gln Glu Lys Glu Ser Gly Pro Leu Thr Arg Glu Leu Arg Gly Leu						
			915		920		925
	Pro Ser Ser Gln Lys Gln Leu Gly Phe Leu Leu Asp Leu Val Cys Arg						
			930		935		940
55	His Thr Ala Val Val Leu Gly Leu Asp Thr Ala Ala Glu Val Asp Pro						

EP 0 791 655 A2

	945	950	955	960
	Asp Leu Ser Phe Lys Lys Gln Gly Ile Gln Ser Met Thr Gly Val Glu			
	965		970	975
5	Leu Arg Asn Arg Leu Leu Thr Glu Thr Gly Leu Ala Leu Pro Thr Thr			
	980	985		990
	Leu Val Tyr Asp Arg Pro Thr Pro Arg Ala Leu Ala Gln Phe Leu His			
10	995	1000		1005
	Thr Glu Leu Leu Asp Gly Ser Pro Ser Gly Ser Val Leu Ala Pro Ala			
	1010	1015		1020
	Gln Lys Ser Phe Glu Ala Gly Gly Pro Gly Val Leu Ser Ser Ala Ala			
15	1025	1030	1035	1040
	Val Gly Val Ser Asp Ala Arg Gly Gly Ser Arg Asp Asp Asp Asp Pro			
	1045		1050	1055
	Ile Ala Ile Val Gly Val Gly Cys Arg Leu Pro Gly Gly Val Asp Ser			
20	1060	1065		1070
	Arg Ala Ala Leu Trp Glu Leu Leu Glu Ser Gly Ala Asp Ala Ile Ser			
	1075	1080		1085
	Ser Phe Pro Thr Asp Arg Gly Trp Asp Leu Asp Gly Leu Tyr Asp Pro			
25	1090	1095		1100
	Glu Pro Gly Thr Pro Gly Lys Thr Tyr Val Arg Glu Gly Gly Phe Leu			
	1105	1110	1115	1120
30	His Ser Ala Ala Glu Phe Asp Ala Glu Phe Phe Gly Ile Ser Pro Arg			
	1125		1130	1135
	Glu Ala Thr Ala Met Asp Pro Gln Gln Arg Leu Leu Leu Glu Ala Ser			
35	1140	1145		1150
	Trp Glu Ala Leu Glu Asp Ala Gly Val Leu Pro Glu Ser Leu Arg Gly			
	1155	1160		1165
	Gly Asp Ala Gly Val Phe Val Gly Ala Thr Ala Pro Glu Tyr Gly Pro			
40	1170	1175		1180
	Arg Leu His Glu Gly Ala Asp Gly Tyr Glu Gly Tyr Leu Leu Thr Gly			
	1185	1190	1195	1200
	Thr Thr Ala Ser Val Ala Ser Gly Arg Ile Ala Tyr Thr Leu Gly Thr			
45	1205	1210		1215
	Gly Gly Pro Ala Leu Thr Val Asp Thr Ala Cys Ser Ser Ser Leu Val			
	1220	1225		1230
	Ala Leu His Leu Ala Val Gln Ala Leu Arg Arg Gly Glu Cys Gly Leu			
50	1235	1240		1245
	Ala Leu Ala Gly Gly Ala Thr Val Met Ser Gly Pro Gly Met Phe Val			
	1250	1255		1260
55	Glu Phe Ser Arg Gln Arg Gly Leu Ala Pro Asp Gly Arg Cys Met Pro			

EP 0 791 655 A2

	1265	1270	1275	1280
	Phe Ser Ala Asp	Ala Asp Gly Thr Ala Trp Ser	Glu Gly Val Ala Val	
		1285	1290	1295
5	Leu Ala Leu Glu Arg	Leu Ser Asp Ala Arg Arg	Ala Gly His Arg Val	
		1300	1305	1310
	Leu Gly Val Val Arg	Gly Ser Ala Val Asn Gln Asp	Gly Ala Ser Asn	
10		1315	1320	1325
	Gly Leu Thr Ala Pro	Asn Arg Ser Ala Gln Glu Gly	Val Ile Arg Ala	
		1330	1335	1340
	Ala Leu Ala Asp Ala	Gly Leu Ala Pro Gly Asp Val	Asp Ala Val Glu	
15		1345	1350	1355
	Ala His Gly Thr Gly	Thr Ala Leu Gly Asp Pro Ile	Glu Ala Ser Ala	
		1365	1370	1375
	Leu Leu Ala Thr Tyr	Gly Arg Glu Arg Val Gly Asp	Pro Leu Trp Leu	
20		1380	1385	1390
	Gly Ser Leu Lys Ser	Asn Val Gly His Thr Gln Ala	Ala Ala Gly Ala	
		1395	1400	1405
	Ala Gly Val Val Lys	Met Leu Leu Ala Leu Glu His	Gly Thr Leu Pro	
25		1410	1415	1420
	Arg Thr Leu His Ala	Asp Arg Pro Ser Thr His Val	Asp Trp Ser Ser	
		1425	1430	1435
	Gly Thr Val Ala Leu	Leu Ala Glu Ala Arg Arg Trp	Pro Arg Arg Ser	
30		1445	1450	1455
	Asp Arg Pro Arg Arg	Ala Ala Val Ser Ser Phe Gly	Ile Ser Gly Thr	
		1460	1465	1470
	Asn Ala His Leu Ile	Ile Glu Glu Ala Pro Glu Trp	Val Glu Asp Ile	
		1475	1480	1485
	Asp Gly Val Ala Ala	Pro Asp Arg Gly Thr Ala Asp	Ala Ala Ala Pro	
40		1490	1495	1500
	Ser Pro Leu Leu Leu	Ser Ala Arg Ser Glu Gly Ala	Leu Arg Ala Gln	
		1505	1510	1515
	Ala Val Arg Leu Gly	Glu Tyr Val Glu Arg Val Gly	Ala Asp Pro Arg	
45		1525	1530	1535
	Asp Val Ala Tyr Ser	Leu Ala Ser Thr Arg Thr Leu	Phe Glu His Arg	
		1540	1545	1550
	Ala Val Val Pro Cys	Gly Gly Arg Gly Glu Leu Val	Ala Ala Leu Gly	
50		1555	1560	1565
	Gly Phe Ala Ala Gly	Arg Val Ser Gly Gly Val Arg	Ser Gly Arg Ala	
		1570	1575	1580
55	Val Pro Gly Gly Val	Gly Val Leu Phe Thr Gly Gln	Gly Ala Gln Trp	

EP 0 791 655 A2

	1585	1590	1595	1600
5	Val Gly Met Gly Arg Gly Leu Tyr Ala Gly Gly Gly Val Phe Ala Glu	1605	1610	1615
	Val Leu Asp Glu Val Leu Ser Met Val Gly Glu Val Asp Gly Arg Ser	1620	1625	1630
10	Leu Arg Asp Val Met Phe Gly Asp Val Asp Val Asp Ala Gly Ala Gly	1635	1640	1645
	Ala Asp Ala Gly Ala Gly Ala Gly Ala Gly Val Gly Ser Gly Ser Gly	1650	1655	1660
15	Ser Val Gly Gly Leu Leu Gly Arg Thr Glu Phe Ala Gln Pro Ala Leu	1665	1670	1675
	Phe Ala Leu Glu Val Ala Leu Phe Arg Ala Leu Glu Ala Arg Gly Val	1685	1690	1695
20	Glu Val Ser Val Val Leu Gly His Ser Val Gly Glu Val Ala Ala Ala	1700	1705	1710
	Tyr Val Ala Gly Val Leu Ser Leu Gly Asp Ala Val Arg Leu Val Val	1715	1720	1725
25	Ala Arg Gly Gly Leu Met Gly Gly Leu Pro Val Gly Gly Gly Met Trp	1730	1735	1740
	Ser Val Gly Ala Ser Glu Ser Val Val Arg Gly Val Val Glu Gly Leu	1745	1750	1755
30	Gly Glu Trp Val Ser Val Ala Ala Val Asn Gly Pro Arg Ser Val Val	1765	1770	1775
	Leu Ser Gly Asp Val Gly Val Leu Glu Ser Val Val Ala Ser Leu Met	1780	1785	1790
35	Gly Asp Gly Val Glu Cys Arg Arg Leu Asp Val Ser His Gly Phe His	1795	1800	1805
	Ser Val Leu Met Glu Pro Val Leu Gly Glu Phe Arg Gly Val Val Glu	1810	1815	1820
40	Ser Leu Glu Phe Gly Arg Val Arg Pro Gly Val Val Val Val Ser Gly	1825	1830	1835
	Val Ser Gly Gly Val Val Gly Ser Gly Glu Leu Gly Asp Pro Gly Tyr	1845	1850	1855
45	Trp Val Arg His Ala Arg Glu Ala Val Arg Phe Ala Asp Gly Val Gly	1860	1865	1870
50	Val Val Arg Gly Leu Gly Val Gly Thr Leu Val Glu Val Gly Pro His	1875	1880	1885
	Gly Val Leu Thr Gly Met Ala Gly Glu Cys Leu Gly Ala Gly Asp Asp	1890	1895	1900
55	Val Val Val Val Pro Ala Met Arg Arg Gly Arg Ala Glu Arg Glu Val			

EP 0 791 655 A2

	1905	1910	1915	1920
	Phe Glu Ala Ala Leu Ala Thr Val Phe Thr Arg Asp Ala Gly Leu Asp	1925	1930	1935
5	Ala Thr Ala Leu His Thr Gly Ser Thr Gly Arg Arg Ile Asp Leu Pro	1940	1945	1950
	Thr Tyr Pro Phe Gln Arg Asp Arg Tyr Trp Leu Asp Pro Val Arg Thr	1955	1960	1965
10	Ala Val Thr Gly Val Glu Pro Ala Gly Ser Pro Ala Asp Ala Arg Ala	1970	1975	1980
	Thr Glu Arg Gly Arg Ser Thr Thr Ala Gly Ile Arg Tyr Arg Val Ala	1985	1990	1995
15	Trp Gln Pro Ala Val Val Asp Arg Gly Asn Pro Gly Pro Ala Gly His	2005	2010	2015
	Val Leu Leu Leu Ala Pro Asp Glu Asp Thr Ala Asp Ser Gly Leu Ala	2020	2025	2030
20	Pro Ala Ile Ala Arg Glu Leu Ala Val Arg Gly Ala Glu Val His Thr	2035	2040	2045
	Val Ala Val Pro Val Gly Thr Gly Arg Glu Ala Ala Gly Asp Leu Leu	2050	2055	2060
25	Arg Ala Ala Gly Asp Gly Ala Ala Arg Ser Thr Arg Val Leu Trp Leu	2065	2070	2075
30	Ala Pro Ala Glu Pro Asp Ala Ala Asp Ala Val Ala Leu Val Gln Ala	2085	2090	2095
	Leu Gly Glu Ala Val Pro Glu Ala Pro Leu Trp Ile Thr Thr Arg Glu	2100	2105	2110
35	Ala Ala Ala Val Arg Pro Asp Glu Thr Pro Ser Val Gly Gly Ala Gln	2115	2120	2125
	Leu Trp Gly Leu Gly Gln Val Ala Ala Leu Glu Leu Gly Arg Arg Trp	2130	2135	2140
40	Gly Gly Leu Ala Asp Leu Pro Gly Ser Ala Ser Pro Ala Val Leu Arg	2145	2150	2155
	Thr Phe Val Gly Ala Leu Leu Ala Gly Gly Glu Asn Gln Phe Ala Val	2165	2170	2175
45	Arg Pro Ser Gly Val His Val Arg Arg Val Val Pro Ala Pro Val Pro	2180	2185	2190
	Val Pro Ala Ser Ala Arg Thr Val Thr Thr Ala Pro Ala Thr Ala Val	2195	2200	2205
50	Gly Glu Asp Ala Arg Asn Asp Thr Ser Asp Val Val Val Pro Asp Asp	2210	2215	2220
55	Arg Trp Ser Ser Gly Thr Val Leu Ile Thr Gly Gly Thr Gly Ala Leu			

EP 0 791 655 A2

	2225	2230	2235	2240
	Gly Ala Gln Val	Ala Arg Arg Leu	Ala Arg Ser Gly	Ala Ala Arg Leu
		2245	2250	2255
5	Leu Leu Val Gly	Arg Arg Gly	Ala Ala Gly	Pro Gly Val Gly Glu Leu
		2260	2265	2270
	Val Glu Glu Leu	Thr Ala Leu	Gly Ser Glu	Val Ala Val Glu Ala Cys
10		2275	2280	2285
	Asp Val Ala Asp	Arg Asp Ala	Leu Ala Ala	Leu Leu Ala Gly Leu Pro
		2290	2295	2300
	Glu Glu Arg Pro	Leu Val Ala	Val Leu His	Ala Ala Gly Val Leu Asp
15		2305	2310	2315
	Asp Gly Val Leu	Asp Ser Leu	Thr Ser Asp	Arg Val Asp Ala Val Leu
		2325	2330	2335
	Arg Asp Lys Val	Thr Ala Ala	Arg His Leu	Asp Glu Leu Thr Ala Asp
20		2340	2345	2350
	Leu Pro Leu Asp	Ala Phe Val	Leu Phe Ser	Ser Ile Val Gly Val Trp
		2355	2360	2365
	Gly Asn Gly Gly	Gln Ala Val	Tyr Ala Ala	Ala Asn Ala Ala Leu Asp
25		2370	2375	2380
	Ala Leu Ala Gln	Arg Arg Arg	Ala Arg Gly	Ala Arg Ala Ala Ser Ile
		2385	2390	2395
30				2400
	Ala Trp Gly Pro	Trp Ala Gly	Ala Gly Met	Ala Ser Gly Thr Ala Ala
		2405	2410	2415
	Lys Ser Phe Glu	Arg Asp Gly	Val Thr Ala	Leu Asp Pro Glu Arg Ala
35		2420	2425	2430
	Leu Asp Val Leu	Asp Asp Val	Val Gly Ala	Gly Gly Thr Ser Ala Ala
		2435	2440	2445
	Gly Thr His Ala	Ala Ala Gly	Glu Ser Ser	Leu Leu Val Ala Asp Val Asp
40		2450	2455	2460
	Trp Glu Thr Phe	Val Gly Arg	Ser Val Thr	Arg Arg Thr Trp Ser Leu
		2465	2470	2475
				2480
	Phe Asp Gly Val	Ser Ala Ala	Arg Ser Ala	Arg Ala Gly His Ala Ala
45		2485	2490	2495
	Asp Asp Arg Ala	Ala Leu Thr	Pro Gly Thr	Arg Pro Gly Asp Gly Ala
		2500	2505	2510
	Pro Gly Gly Ser	Gly Gln Asp	Gly Gly Glu	Gly Arg Pro Trp Leu Ser
50		2515	2520	2525
	Val Gly Pro Ser	Pro Ala Glu	Arg Arg Arg	Ala Leu Leu Thr Leu Val
		2530	2535	2540
55				
	Arg Ser Glu Ala	Ala Gly Ile	Leu Arg His	Ala Ser Ala Asp Ala Val

EP 0 791 655 A2

	2545	2550	2555	2560
	Asp Pro Glu Leu Ala Phe Arg Ser Ala Gly Phe Asp Ser Leu Thr Val			
		2565	2570	2575
5	Leu Glu Leu Arg Asn Arg Leu Thr Ala Ala Thr Gly Leu Asn Leu Pro			
		2580	2585	2590
	Asn Thr Leu Leu Phe Asp His Pro Thr Pro Leu Ser Leu Ala Ser His			
10		2595	2600	2605
	Leu His Asp Glu Leu Phe Gly Pro Asp Ser Glu Ala Glu Pro Ala Ala			
		2610	2615	2620
	Ala Ala Pro Thr Pro Val Met Ala Asp Glu Arg Glu Pro Ile Ala Ile			
15		2625	2630	2635
	Val Gly Met Ala Cys Arg Tyr Pro Gly Gly Val Ala Ser Pro Asp Asp			
		2645	2650	2655
	Leu Trp Asp Leu Val Ala Gly Asp Gly His Thr Leu Ser Pro Phe Pro			
20		2660	2665	2670
	Ala Asp Arg Gly Trp Asp Val Glu Gly Leu Tyr Asp Pro Glu Pro Gly			
		2675	2680	2685
	Val Pro Gly Lys Ser Tyr Val Arg Glu Gly Gly Phe Leu Arg Ser Ala			
25		2690	2695	2700
	Ala Glu Phe Asp Ala Glu Phe Phe Gly Ile Ser Pro Arg Glu Ala Thr			
		2705	2710	2715
30				2720
	Ala Met Asp Pro Gln Gln Arg Leu Leu Leu Glu Thr Ser Trp Glu Ala			
		2725	2730	2735
	Leu Glu Arg Ala Gly Ile Val Pro Asp Ser Leu Arg Gly Thr Arg Thr			
35		2740	2745	2750
	Gly Val Phe Ser Gly Ile Ser Gln Gln Asp Tyr Ala Thr Gln Leu Gly			
		2755	2760	2765
	Asp Ala Ala Asp Thr Tyr Gly Gly His Val Leu Thr Gly Thr Leu Gly			
40		2770	2775	2780
	Ser Val Ile Ser Gly Arg Val Ala Tyr Ala Leu Gly Leu Glu Gly Pro			
		2785	2790	2795
				2800
	Ala Leu Thr Val Asp Thr Ala Cys Ser Ser Ser Leu Val Ala Leu His			
45		2805	2810	2815
	Leu Ala Val Gln Ser Leu Arg Arg Gly Glu Cys Asp Leu Ala Leu Ala			
		2820	2825	2830
	Gly Gly Val Thr Val Met Ala Thr Pro Thr Val Phe Val Glu Phe Ser			
50		2835	2840	2845
	Arg Gln Arg Gly Leu Ala Ala Asp Gly Arg Cys Lys Ala Phe Ala Glu			
		2850	2855	2860
55	Gly Ala Asp Gly Thr Ala Trp Ala Glu Gly Val Gly Val Leu Leu Val			

EP 0 791 655 A2

	2865	2870	2875	2880
	Glu Arg Leu Ser Asp Ala Arg Arg Asn Gly His Arg Val Leu Ala Val			
	2885		2890	2895
5	Val Arg Gly Ser Ala Val Asn Gln Asp Gly Ala Ser Asn Gly Leu Thr			
	2900		2905	2910
	Ala Pro Ser Gly Pro Ala Gln Gln Arg Val Ile Arg Glu Ala Leu Ala			
10	2915		2920	2925
	Asp Ala Gly Leu Val Pro Ala Asp Val Asp Val Val Glu Ala His Gly			
	2930		2935	2940
	Thr Gly Thr Ala Leu Gly Asp Pro Ile Glu Ala Gly Ala Leu Leu Ala			
15	2945		2950	2955
	Thr Tyr Gly Arg Glu Arg Val Gly Asp Pro Leu Trp Leu Gly Ser Leu			
			2970	2975
	Lys Ser Asn Ile Gly His Ala Gln Ala Ala Gly Val Gly Gly Val			
20			2985	2990
	Ile Lys Val Val Gln Gly Met Arg His Gly Ser Leu Pro Arg Thr Leu			
			3000	3005
	His Val Asp Ala Pro Ser Ser Lys Val Glu Trp Ala Ser Gly Ala Val			
25			3015	3020
	Glu Leu Leu Thr Glu Thr Arg Ser Trp Pro Arg Arg Val Glu Arg Val			
	3025		3030	3035
30				3040
	Arg Arg Ala Ala Val Ser Ala Phe Gly Val Ser Gly Thr Asn Ala His			
			3050	3055
	Val Val Leu Glu Glu Ala Pro Ala Glu Ala Gly Ser Glu His Gly Asp			
			3065	3070
35				
	Gly Pro Glu Pro Glu Arg Pro Asp Ala Val Thr Gly Pro Leu Ser Trp			
			3080	3085
	Val Leu Ser Ala Arg Ser Glu Gly Ala Leu Arg Ala Gln Ala Val Arg			
40			3095	3100
	Leu Arg Glu Cys Val Glu Arg Val Gly Ala Asp Pro Arg Asp Val Ala			
	3105		3110	3115
				3120
	Gly Ser Leu Val Val Ser Arg Ala Ser Phe Gly Glu Arg Ala Val Val			
45			3130	3135
	Val Gly Arg Gly Arg Glu Glu Leu Leu Ala Gly Leu Asp Val Val Ala			
			3145	3150
	Ala Gly Ala Pro Val Gly Val Ser Ser Gly Ala Gly Ala Val Val Arg			
50			3160	3165
	Gly Ser Ala Val Arg Gly Arg Gly Val Gly Val Leu Phe Thr Gly Gln			
	3170		3175	3180
55				
	Gly Ala Gln Trp Val Gly Met Gly Arg Gly Leu Tyr Ala Gly Gly Gly			

EP 0 791 655 A2

	3185		3190		3195		3200
	Val Phe Ala Glu	Val Leu Asp Glu	Val Leu Ser Val	Val Gly Glu Val			
		3205		3210		3215	
5	Asp Gly Arg Ser	Leu Arg Asp	Val Met Phe Ala	Asp Ala Asp	Ser Val		
		3220		3225		3230	
	Leu Gly Gly Leu	Leu Gly Arg Thr	Glu Phe Ala Gln	Pro Ala Leu Phe			
		3235		3240		3245	
10	Ala Leu Glu Val	Ala Leu Phe Arg	Ala Leu Glu Ala	Arg Gly Val Glu			
		3250		3255		3260	
	Val Ser Val Val	Leu Gly His Ser	Val Gly Glu Val	Ala Ala Ala Tyr			
	3265		3270		3275		3280
	Val Ala Gly Val	Leu Ser Leu Gly	Asp Ala Val Arg	Leu Val Val Ala			
		3285		3290		3295	
20	Arg Gly Gly Leu	Met Gly Gly Leu	Pro Val Gly Gly	Gly Gly Met Trp	Ser		
		3300		3305		3310	
	Val Gly Ala Ser	Glu Ser Val Val	Arg Gly Val Val	Glu Gly Leu Gly			
		3315		3320		3325	
25	Glu Trp Val Ser	Val Ala Ala Val	Asn Gly Pro Arg	Ser Val Val Leu			
		3330		3335		3340	
	Ser Gly Asp Val	Gly Val Leu Glu	Ser Val Val Val	Thr Leu Met Gly			
	3345		3350		3355		3360
30	Asp Gly Val Glu	Cys Arg Arg Leu	Asp Val Ser His	Gly Phe His Ser			
		3365		3370		3375	
	Val Leu Met Glu	Pro Val Leu Gly	Glu Phe Arg Gly	Val Val Glu Ser			
		3380		3385		3390	
35	Leu Glu Phe Gly	Arg Val Arg Pro	Gly Val Val Val	Val Ser Gly Val			
		3395		3400		3405	
	Ser Gly Gly Val	Val Gly Ser Gly	Glu Leu Gly Asp	Pro Gly Tyr Trp			
	3410		3415		3420		
40	Val Arg His Ala	Arg Glu Ala Val	Arg Phe Ala Asp	Gly Val Gly Val			
	3425		3430		3435		3440
	Val Arg Gly Leu	Gly Val Gly Thr	Leu Val Glu Val	Gly Pro His Gly			
		3445		3450		3455	
45	Val Leu Thr Gly	Met Ala Gly Gln	Cys Leu Glu Ala	Gly Asp Asp Val			
		3460		3465		3470	
50	Val Val Val Pro	Ala Met Arg Arg	Gly Arg Pro Glu	Arg Glu Val Phe			
		3475		3480		3485	
	Glu Ala Ala Leu	Ala Thr Val Phe	Thr Arg Asp Ala	Gly Leu Asp Ala			
		3490		3495		3500	
55	Thr Thr Leu His	Thr Gly Ser Thr	Gly Arg Arg Ile	Asp Leu Pro Thr			

EP 0 791 655 A2

	3505	3510	3515	3520
	Tyr Pro Phe Gln His Asn Arg Tyr Trp	Ala Thr Gly Ser Val Thr Gly		
	3525	3530	3535	
5	Ala Thr Gly Thr Ser Ala Ala Ala Arg Phe Gly Leu Glu Trp Lys Asp			
	3540	3545	3550	
	His Pro Phe Leu Ser Gly Ala Thr Pro Ile Ala Gly Ser Gly Ala Leu			
10	3555	3560	3565	
	Leu Leu Thr Gly Arg Val Gly Leu Ala Ala His Pro Trp Leu Ala Asp			
	3570	3575	3580	
	His Ala Ile Ser Gly Thr Val Leu Leu Pro Gly Thr Ala Ile Ala Asp			
15	3585	3590	3595	3600
	Leu Leu Leu Arg Ala Val Glu Glu Val Gly Ala Gly Gly Val Glu Glu			
	3605	3610	3615	
	Leu Thr Leu His Glu Pro Leu Leu Leu Pro Glu Arg Gly Gly Leu His			
20	3620	3625	3630	
	Val Gln Val Leu Val Glu Ala Ala Asp Glu Gln Gly Arg Arg Ala Val			
	3635	3640	3645	
	Ala Val Ala Ala Arg Pro Glu Gly Pro Gly Arg Asp Gly Glu Glu Gln			
25	3650	3655	3660	
	Glu Trp Thr Arg His Ala Glu Gly Val Leu Thr Ser Thr Glu Thr Ala			
	3665	3670	3675	3680
30	Val Pro Asp Met Gly Trp Ala Ala Gly Ala Trp Pro Pro Pro Gly Ala			
	3685	3690	3695	
	Glu Pro Ile Asp Val Glu Glu Leu Tyr Asp Ala Phe Ala Ala Asp Gly			
	3700	3705	3710	
	Tyr Gly Tyr Gly Pro Ala Phe Thr Ala Leu Ser Gly Val Trp Arg Leu			
	3715	3720	3725	
	Gly Asp Glu Leu Phe Ala Glu Val Arg Arg Pro Ala Gly Gly Ala Gly			
40	3730	3735	3740	
	Thr Thr Gly Asp Gly Phe Gly Val His Pro Ala Leu Phe Asp Ala Ala			
	3745	3750	3755	3760
	Leu His Pro Trp Arg Ala Gly Gly Leu Leu Pro Asp Thr Gly Gly Thr			
45	3765	3770	3775	
	Thr Trp Ala Pro Phe Ser Trp Gln Gly Ile Ala Leu His Thr Thr Gly			
	3780	3785	3790	
	Ala Glu Thr Leu Arg Val Arg Leu Ala Pro Ala Ala Gly Gly Thr Glu			
50	3795	3800	3805	
	Ser Ala Phe Ser Val Gln Ala Ala Asp Pro Ala Gly Thr Pro Val Leu			
	3810	3815	3820	
55	Thr Leu Asp Ala Leu Leu Leu Arg Pro Val Thr Leu Gly Arg Ala Asp			

EP 0 791 655 A2

	3825	3830	3835	3840
	Ala Pro Gln Pro Leu Tyr Arg Val Asp Trp Gln Pro Val Gly Gln Gly			
		3845	3850	3855
5	Thr Glu Ala Ser Gly Ala Gln Gly Trp Thr Val Leu Gly Gln Ala Ala			
		3860	3865	3870
	Ala Glu Thr Val Ala Gln Pro Ala Ala His Ala Asp Leu Thr Ala Leu			
10		3875	3880	3885
	Arg Thr Ala Val Ala Ala Ala Gly Thr Pro Val Pro Arg Leu Val Val			
		3890	3895	3900
	Val Ser Pro Val Asp Thr Arg Leu Asp Glu Gly Pro Val Leu Ala Asp			
15		3905	3910	3915
	Ala Glu Ala Arg Ala Arg Ala Gly Asp Gly Trp Asp Asp Asp Pro Leu			
		3925	3930	3935
	Arg Val Ala Leu Gly Arg Gly Leu Thr Leu Val Arg Glu Trp Val Glu			
20		3940	3945	3950
	Asp Glu Arg Leu Ala Asp Ser Arg Leu Val Val Leu Thr Arg Gly Ala			
		3955	3960	3965
	Val Ala Ala Gly Pro Gly Asp Val Pro Asp Leu Thr Gly Ala Ala Leu			
25		3970	3975	3980
	Trp Gly Leu Leu Arg Ser Ala Gln Ser Glu Tyr Pro Asp Arg Phe Thr			
		3985	3990	3995
30				4000
	Leu Ile Asp Val Asp Asp Ser Pro Glu Ser Arg Ala Ala Leu Pro Arg			
		4005	4010	4015
	Ala Leu Gly Ser Ala Glu Arg Gln Leu Ala Leu Arg Thr Gly Asp Val			
35		4020	4025	4030
	Leu Ala Pro Ala Leu Val Pro Met Ala Thr Arg Pro Ala Glu Thr Thr			
		4035	4040	4045
	Pro Ala Thr Ala Val Ala Ser Ala Thr Thr Gln Thr Gln Val Thr Ala			
40		4050	4055	4060
	Pro Ala Pro Asp Asp Pro Ala Ala Asp Ala Val Phe Asp Pro Ala Gly			
		4065	4070	4075
	Thr Val Leu Ile Thr Gly Gly Thr Gly Ala Leu Gly Arg Arg Val Ala			
45		4085	4090	4095
	Ser His Leu Ala Arg Arg Tyr Gly Val Arg His Met Leu Leu Val Ser			
		4100	4105	4110
	Arg Arg Gly Pro Asp Ala Pro Glu Ala Gly Pro Leu Glu Arg Glu Leu			
50		4115	4120	4125
	Ala Gly Leu Gly Val Thr Ala Thr Phe Leu Ala Cys Asp Leu Thr Asp			
		4130	4135	4140
55	Ile Glu Ala Val Arg Lys Ala Val Ala Ala Val Pro Ser Asp His Pro			

EP 0 791 655 A2

	4145		4150		4155		4160
5	Leu Thr Gly	Val Val His Thr	Ala Gly	Val Leu Asp	Asp Gly	Ala Leu	
		4165		4170		4175	
	Thr Gly Leu	Thr Arg Gln Arg	Leu Asp Thr	Val Leu Arg	Pro Lys	Ala	
		4180		4185		4190	
10	Asp Ala Val	Arg Asn Leu His	Glu Ala Thr	Leu Asp Arg	Pro Leu Arg		
		4195		4200		4205	
	Ala Phe Val	Leu Phe Ser Ala	Ala Ala Gly	Leu Leu Gly	Arg Pro Gly		
		4210		4215		4220	
15	Gln Ala Ser	Tyr Ala Ala Ala	Asn Ala Val	Leu Asp Ala	Leu Ala Gly		
		4225		4230		4235	
						4240	
	Ala Arg Arg	Ala Ala Gly	Leu Pro Ala	Val Ser Leu	Ala Trp Gly	Leu	
		4245		4250		4255	
20	Trp Asp Glu	Gln Thr Gly	Met Ala Gly	Gly Leu Asp	Glu Met Ala	Leu	
		4260		4265		4270	
	Arg Val Leu	Arg Arg Asp	Gly Ile Ala	Ala Met Pro	Pro Glu Gln	Gly	
25		4275		4280		4285	
	Leu Glu Leu	Leu Asp Leu	Ala Leu Thr	Gly His Arg	Asp Gly Pro	Ala	
		4290		4295		4300	

30

35

40

45

50

55

EP 0 791 655 A2

Val Leu Val Pro Leu Leu Leu Asp Gly Ala Ala Leu Arg Arg Thr Ala
4305 4310 4315 4320

5 Lys Glu Arg Gly Ala Ala Thr Met Ser Pro Leu Leu Arg Ala Leu Leu
4325 4330 4335

Pro Ala Ala Leu Arg Arg Ser Gly Gly Ala Gly Ala Pro Ala Ala Ala
4340 4345 4350

10 Asp Arg His Gly Lys Glu Ala Asp Pro Gly Ala Gly Arg Leu Ala Gly
4355 4360 4365

Met Val Ala Leu Glu Ala Ala Glu Arg Ser Ala Ala Val Leu Glu Leu
4370 4375 4380

15 Val Thr Glu Gln Val Ala Glu Val Leu Gly Tyr Ala Ser Ala Ala Glu
4385 4390 4395 4400

Ile Glu Pro Glu Arg Pro Phe Arg Glu Ile Gly Val Asp Ser Leu Ala
20 4405 4410 4415

Ala Val Glu Leu Arg Asn Arg Leu Ser Arg Leu Val Gly Leu Arg Leu
4420 4425 4430

25 Pro Thr Thr Leu Ser Phe Asp His Pro Thr Pro Lys Asp Met Ala Gln
4435 4440 4445

His Ile Asp Gly Gln Leu Pro Arg Pro Ala Gly Ala Ser Pro Ala Asp
4450 4455 4460

30 Ala Ala Leu Glu Gly Ile Gly Asp Leu Ala Arg Ala Val Ala Leu Leu
4465 4470 4475 4480

Gly Thr Gly Asp Ala Arg Arg Ala Glu Val Arg Glu Gln Leu Val Gly
4485 4490 4495

35 Leu Leu Ala Ala Leu Asp Pro Pro Gly Arg Thr Gly Thr Ala Ala Pro
4500 4505 4510

Gly Val Pro Ser Gly Ala Asp Gly Ala Glu Pro Thr Val Thr Asp Arg
40 4515 4520 4525

Leu Asp Glu Ala Thr Asp Asp Glu Ile Phe Ala Phe Leu Asp Glu Gln
4530 4535 4540

45 Leu *
4545

50

55

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CGAGGCCGGC GGGCC

Claims

1. A DNA molecule comprising an isolated DNA sequence that encodes a tyactone synthase domain.
2. The DNA molecule as claimed in Claim 1 wherein the isolated DNA sequence is selected from the group consisting of:
 - nucleotides 942 to 2156, 2571 to 3557, 3675 to 3929, 3993 to 5264, 5631 to 6617, 7410 to 7949, 8220 to 8471, 8541 to 9812, 10260 to 11246, 11319 to 11876, 12861 to 13415, 13719 to 13970, 14411 to 15697, 16055 to 17122, 17198 to 17794, 18584 to 19138, 19415 to 19666, 20136 to 21404, 21771 to 22757, 23541 to 24077, 24360 to 24611, 24675 to 25949, 26292 to 27284, 27360 to 27917, 28767 to 29813, 29829 to 30368, 30651 to 30902, 31337 to 32608, 32975 to 33961, 34694 to 35236, 35492 to 35743, 36360 to 37631, 37989 to 38987, 39759 to 40313, 40575 to 40826, and 41235 to 41333 all in SEQ ID NO:1.
3. The DNA molecule as claimed in Claim 1 wherein the isolated DNA sequence is selected from the group consisting of:
 - nucleotides 942 to 8471, 8541 to 13970, 14411 to 19666, 20136 to 24611, 24675 to 30902, 31337 to 35743, and 36360 to 40826 all in SEQ ID NO:1.
4. The DNA molecule as claimed in Claim 1 wherein the isolated DNA sequence is selected from the group consisting of:
 - nucleotides 816 to 14234, 14351 to 19945, 20010 to 31199, 31232 to 36067, and 36249 to 41774 all in SEQ ID NO:1.
5. The DNA molecule as claimed in Claim 1 wherein the isolated DNA sequence is SEQ ID NO:1.
6. A polypeptide comprising an amino acid sequence that consists of a tyactone synthase domain.
7. The polypeptide of claim 6 wherein the amino acid sequence is selected from the group consisting of:
 - (a) amino acids 43 to 447, 586 to 914, 954 to 1038, 1060 to 1483, 1606 to 1934, 2199 to 2378, 2469 to 2552, 2576 to 2999, 3149 to 3477, 3502 to 3687, 4016 to 4200, and 4302 to 4385 in SEQ ID NO:2;
 - (b) amino acids 21 to 449, 569 to 924, 950 to 1148, 1412 to 1596, and 1689 to 1772 in SEQ ID NO:3;
 - (c) amino acids 43 to 465, 588 to 916, 1178 to 1356, and 1451 to 1534, 1556 to 1980, 2095 to 2425, 2451 to 2636, 3274 to 3453, and 3548 to 3631 in SEQ ID NO:4;
 - (d) amino acids 36 to 459, 582 to 910, 1155 to 1335, and 1421 to 1504 in SEQ ID NO:5; and
 - (e) amino acids 38 to 461, 581 to 913, 1171 to 1355, 1443 to 1526, and 1663 to 1695 in SEQ ID NO:6.
8. The polypeptide of claim 6 wherein the amino acid sequence is selected from the group consisting of:
 - (a) amino acids 1060 to 2552 and 2576 to 4385 in SEQ ID NO:2;
 - (b) amino acids 21 to 1772 in SEQ ID NO:3;

- (c) amino acids 43 to 1534 and 1556 to 3631 in SEQ ID NO:4;
- (d) amino acids 36 to 1504 in SEQ ID NO:5; and
- (e) amino acids 38 to 1526 in SEQ ID NO:6.

- 5 **9.** The polypeptide of claim 6 wherein the amino acid sequence is selected from the group consisting of SEQ ID NO: 2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, and SEQ ID NO:6.
- 10 **10.** A recombinant DNA vector comprising a DNA molecule of Claim 1.
- 10 **11.** A recombinant DNA vector comprising a DNA molecule of Claim 2.
- 12 **12.** A recombinant DNA vector comprising a DNA molecule of Claim 3.
- 13 **13.** A recombinant DNA vector comprising a DNA molecule of Claim 4.
- 15 **14.** A recombinant DNA vector comprising a DNA molecule of Claim 5.
- 15 **15.** A recombinant DNA vector of Claim 10 which is NRRL B-18688.
- 20 **16.** A recombinant DNA vector of Claim 10 which is NRRL B-18689
- 17 **17.** A host cell transformed with a recombinant DNA vector of Claim 10.
- 18 **18.** A host cell transformed with a recombinant DNA vector of Claim 11.
- 25 **19.** A host cell transformed with a recombinant DNA vector of Claim 12.
- 20 **20.** A host cell transformed with a recombinant DNA vector of Claim 13.
- 30 **21.** A host cell transformed with a recombinant DNA vector of Claim 14.
- 22 **22.** The DNA molecule as claimed in Claim 1 wherein the isolated DNA sequence is SEQ ID NO:7.
- 35 **23.** The polypeptide of SEQ ID NO:8.

Fig. 1

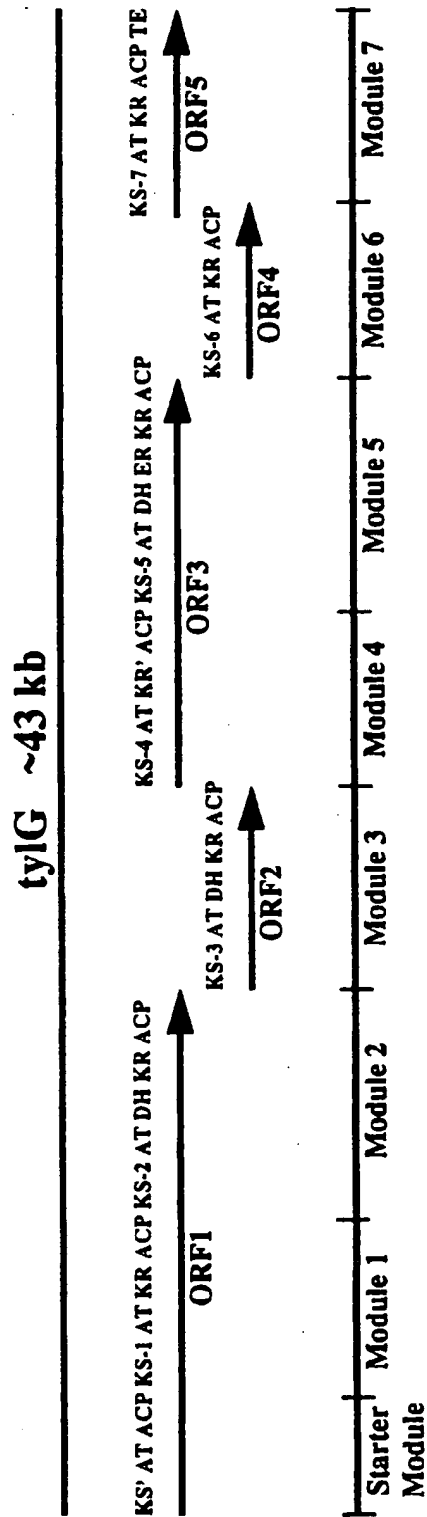


Fig. 2

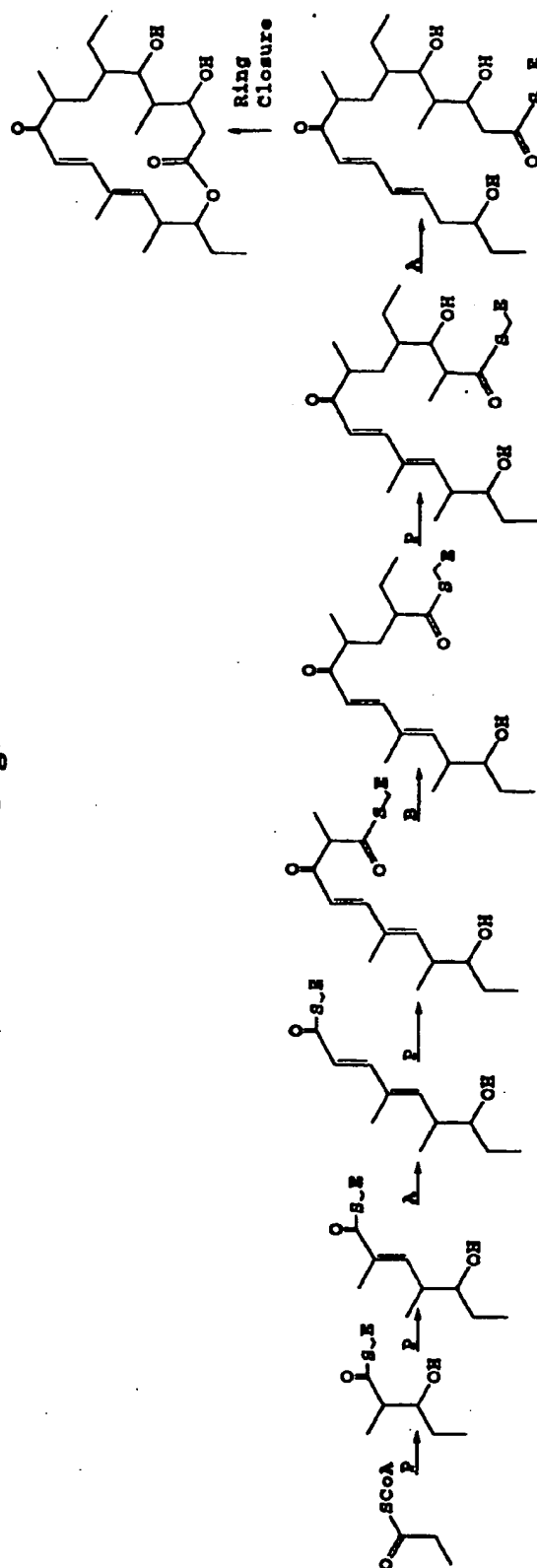


Fig. 3

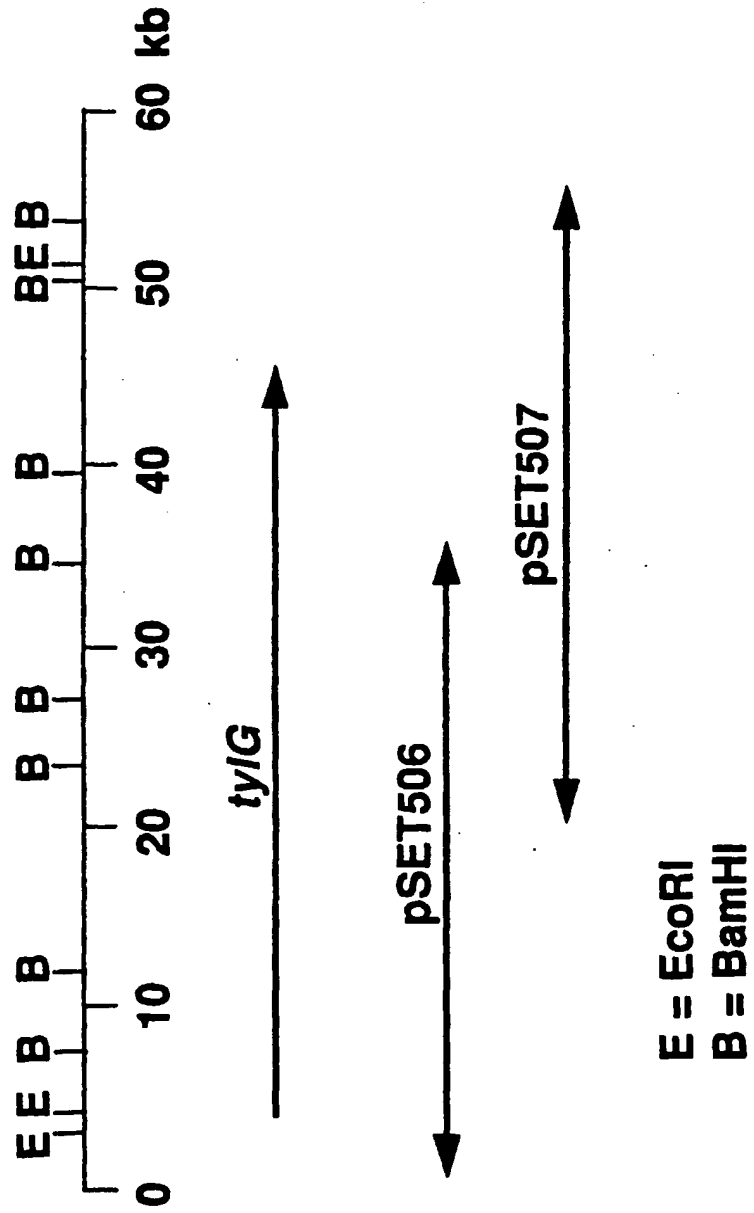


Fig. 4

srmG ~44kb

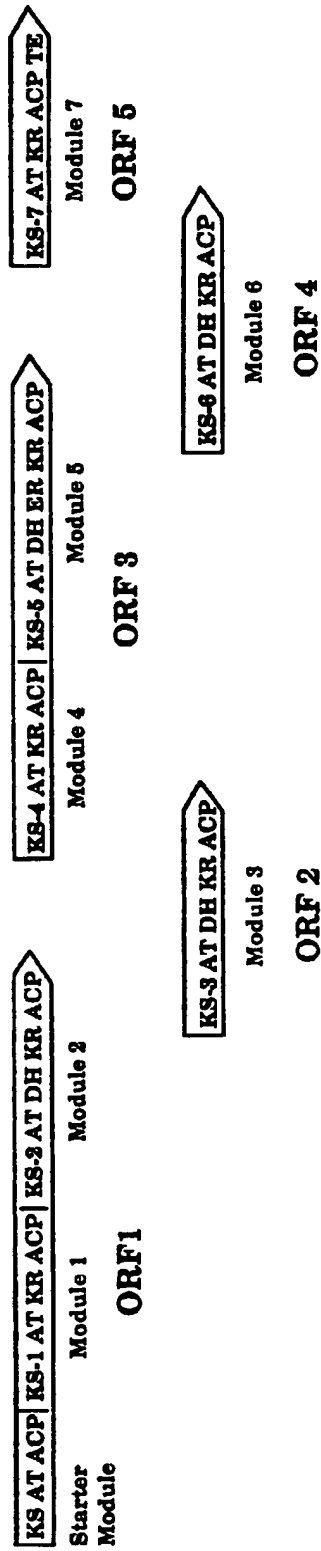


Fig. 5

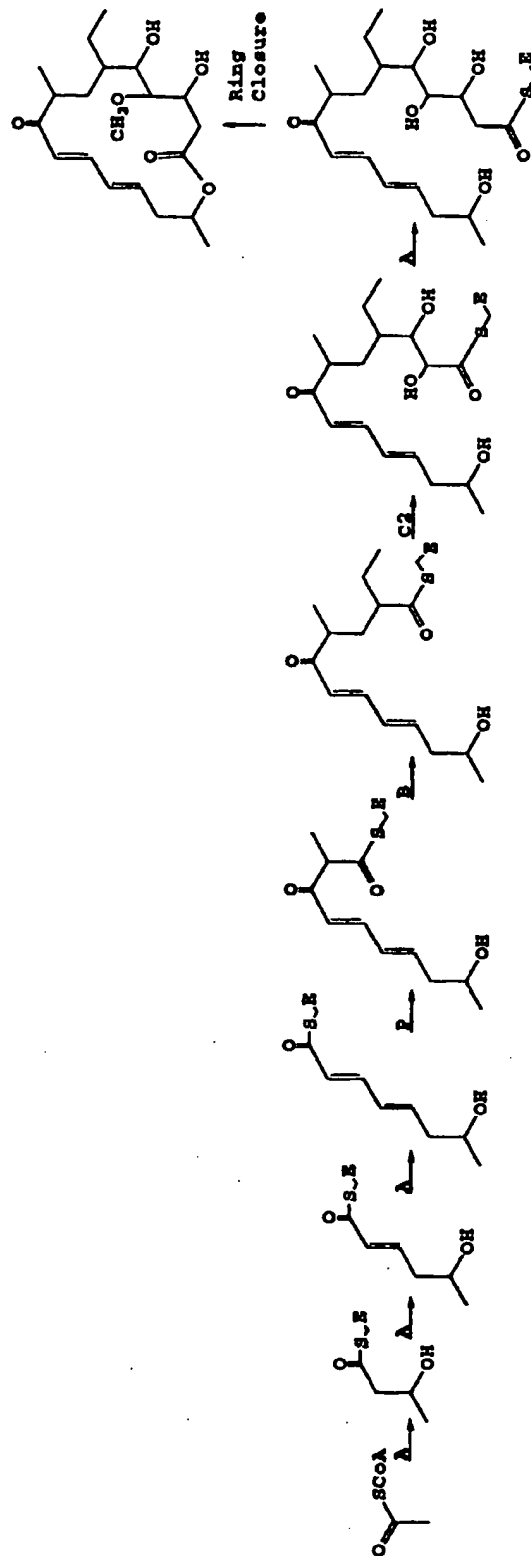
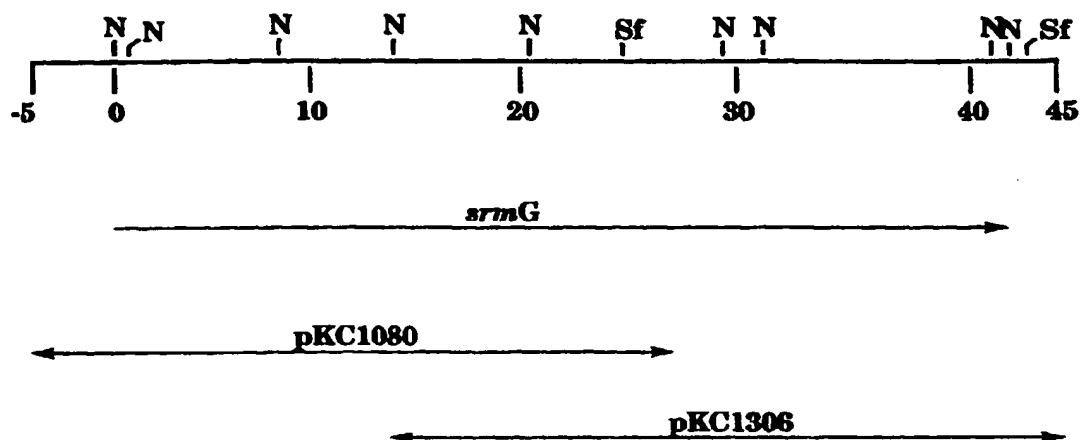


Fig. 6



N = *Nru*I

Sf = *Sfu*I